

						/ug=Hs.81771 /len=1637				
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	NM_002046	12p13		Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (5'_M'_3 represent transcript regions 5 prime, Middle, and 3 prime respectively)				AFFX-HUMGAPDH/M
CTNNAL1 (catenin (cadherin-associated protein), alpha-like 1)	U97067	Hs.58488	NM_003798	9q31.2		Cluster Incl. U97067:Homo sapiens alpha- catenin-like protein mRNA, complete cds /cds=(43,2247) /gb=U97067 /gi=3342777 /ug=Hs.58488 /len=2446				35331_at
GNA15 (guanine nucleotide binding protein (G protein), alpha 15 (Gq class	M63904	Hs.73797	NM_002068	19p13.3		Cluster Incl. M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891 /ug=Hs.73797 /len=2060				40365_at

KCNAB2 (potassium voltage-gated channel, shaker-related subfamily, beta member 2)	AF044253	Hs.298184	NM_003636	1p36.3	Cluster Incl. AF044253: Homo sapiens potassium channel beta 2 subunit (HK1beta2.2) mRNA, alternatively spliced, complete cds /cds=(0,1061) /gb=AF044253 /gi=2827465 /ug=Hs.154417 /len=1062	31901_at
TARS (threonyl-tRNA synthetase)	M63180	Hs.84131	NM_003191	5p13-cen	Cluster Incl. M63180: Human threonyl-tRNA synthetase mRNA, complete cds /cds=(138,2276) /gb=M63180 /gi=339679 /ug=Hs.84131 /len=2644	38473_at
UQCRFS1 (ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1)	L32977	Hs.3712	NM_006003	19q12-q13.1	Cluster Incl. L32977: Homo sapiens (clone f17252) ubiquinol cytochrome c reductase Rieske iron-sulphur protein (UQCRFS1) gene /cds=(90,914) /gb=L32977 /gi=488298 /ug=Hs.3712 /len=1203	34401_at
ONECUT3 (one cut domain, family member 3)	AC004755			19	Cluster Incl. AC004755: Homo sapiens chromosome 19, fosmid /cds=(0,2726) /gb=AC004755 /gi=3165405	33685_at

						/Jug=Hs.184922 /len=2727				
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	NM_002046	12p13		Homo sapiens /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (5' _M_ _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMGAPDH/M			
MAX (MAX protein)	X60287	Hs.42712	NM_002382	14q23		X60287 /FEATURE=cds /DEFINITION=HSMAXM H.sapiens max mRNA	1981_s_at			
SH3GL1 (SH3-domain GRB2-like 1	X99656	Hs.97616	NM_003025	19p13.3		Cluster Incl. X99656:H.sapiens mRNA for protein containing SH3 domain, SH3GL1 /cds=(15,1121) /gb=X99656 /gi=1869809 /Jug=Hs.97616 /len=2349	39159_at			
SFPQ (splicing factor proline/glutamine rich (polypyrimidine tract-binding protein- associated))	W27050	Hs.180610	NM_005066	1pter-p32.3		Cluster Incl. W27050:1977 Homo sapiens cDNA /gb=W27050 /gi=1306422 /Jug=Hs.180610 /len=699	41199_s_at			

PPP6C (protein phosphatase 6, catalytic subunit)	X92972	Hs.80324	NM_002721	xq22.3	Cluster Incl. X92972:H.sapiens mRNA for protein phosphatase 6 /cds=(21,938) /gb=X92972 /gi=5701862 /ug=Hs.80324 /len=1292	37581_at
HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like))	L24521	Hs.89525	NM_004494	xq25	Cluster Incl. L24521:Human transformation-related protein mRNA, 3 end /cds=(0,1108) /gb=L24521 /gi=403459 /ug=Hs.169225 /len=1240	36446_s_at
ACTG1 (actin, gamma 1)	X04098	Hs.14376	NM_001614	17q25	Cluster Incl. X04098:Human mRNA for cytoskeletal gamma-actin /cds=(73,1200) /gb=X04098 /gi=28338 /ug=Hs.234733 /len=1918	34160_at
FBXO7 (F-box only protein 7)	AL050254	Hs.5912	NM_012179	22q11.2-qter	Cluster Incl. AL050254:Novel human gene mapping to chromosome 22 /cds=(205,1773) /gb=AL050254 /gi=4886422 /ug=Hs.5912 /len=2075	35337_at
SCML2 (sex comb on midleg (Drosophila)-like 2)	Y18004	Hs.171558	NM_006089	xp22	Cluster Incl. Y18004:Homo sapiens mRNA for SCML2 protein /cds=(91,2193)	38518_at

							/gb=Y18004 /gi=4480941 /ug=Hs.171558 /len=4130				
UBE2L3 (ubiquitin-conjugating enzyme E2L	S81003	Hs.108104	NM_003347	22q11.21	S81003 /DEFINITION=S81003 - L-UBC=ubiquitin conjugating enzyme [human, odontogenic keratocysts, mRNA Partial, 683 nt]	/FEATURE=	223_at				
GNAQ (guanine nucleotide binding protein (G protein), q polypeptide	U40038	Hs.296261	NM_002072	9q21	Cluster Incl. U40038:Human GTP-binding protein alpha q subunit (GNAQ) mRNA, complete cds /cds=(42,1121) /gb=U40038 /gi=1181670 /ug=Hs.180950 /len=1450		38581_at				
UGTREL7(UDP-glucuronic acid/UDP-N- acetyl/galactosamine dual transporter	D87449	Hs.82635	NM_015139	1	Cluster Incl. D87449:Human mRNA for KJAA0260 gene, partial cds /cds=(0,1153) /gb=D87449 /gi=1665786 /ug=Hs.82635 /len=5918		37888_at				

Table 12:

UC/L/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
KIAA0101(KIAA0101 gene product)	D14657	Hs.81892	NM_014736	15	Cluster Incl. D14657:Human mRNA for KIAA0101 gene, complete cds /cds=(61,396) /gb=D14657 /gi=285938 /ug=Hs.81892 /len=836	38116_at
IGFBP7 (insulin-like growth factor binding protein 7)	L19182	Hs.119206	NM_001553	4q12	L19182 /DEFINITION=HUMMAC25X Human MAC25 mRNA, complete cds	2062_at
RNASE2 (ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin))	X55988	Hs.728	NM_002934	14q24-q31	Cluster Incl. X55988:Human EDN mRNA for eosinophil derived neurotoxin /cds=(71,556) /gb=X55988 /gi=31088 /ug=Hs.728 /len=735	36766_at

SCYC2 (small inducible cytokine subfamily C, member 2)	D63789	Hs.174228	NM_003175	1q23-q25	Cluster Incl. D63789:Homo sapiens DNA for SCM-1beta precursor, complete cds /cds=(21,365) /gb=D63789 /gi=1754608 /ug=Hs.174228 /len=485	31495_at
DEFA1 (defensin, alpha 1, myeloid-related sequence)	AL036554	Hs.274463	NM_004084	8p23.2-p23.1	Cluster Incl. AL036554:DKFZp584J2262_r1 sapiens cDNA, 5 end /clone=DKFZp584J2262 /clone_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.1379 /len=517	31793_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	NM_002046	12p13	Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 /5_/_M_/_3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMGAPDH/M
GSN (gelsolin (amyloidosis, Finnish type))	X04412	Hs.290070	NM_000177	9q33	Cluster Incl. X04412:Human mRNA for plasma gelsolin /cds=(14,2362) /gb=X04412 /gi=35447 /ug=Hs.80562	32812_at

						/len=2602	
GATA2 (GATA-binding protein 2)	M77810	Hs.334695	NM_002050	3q21		M77810 /DEFINITION=HUMGATA2A Human transcription factor GATA-2 (GATA-2) mRNA, complete cds	1072_g_at
HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like))	L24521	Hs.89525	NM_004494	Xq25		Cluster Incl. L24521:Human transformation-related protein mRNA, 3 end /cds=(0,1108) /gb=L24521 /gi=403459 /ug=Hs.169225 /len=1240	38446_s_at
TUBG1 (tubulin, gamma 1)	M61764	Hs.21635	NM_001070	17q21		Cluster Incl. M61764:Human gamma- tubulin mRNA, complete cds /cds=(24,1379) /gb=M61764 /gi=183702 /ug=Hs.21635 /len=1568	33346_r_at
NUDEL(nuclear distribution gene E-like)	AF038203	Hs.3850	NM_030808	17		Cluster Incl. AF038203:Homo sapiens clone 23596 mRNA sequence /cds=UNKNOWN /gb=AF038203 /gi=2795924 /ug=Hs.3850 /len=1473	34413_at

TYMS (thymidylate synthetase)	D00596	Hs.82962	NM_001071	18p11.32	D00596 /DEFINITION=HUMTS1 Homo sapiens gene for thymidylate synthase, exons 1, 2, 3, 4, 5, 6, 7, complete cds	1505_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.189476	NM_002046	12p13	Homo sapiens /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5'_M'_3' represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUMGAP.B/H/M
EZH2 (enhancer of zeste (Drosophila) homolog 2)	U61145	Hs.77256	NM_004456	7q35-q36	Cluster Incl. U61145:Human enhancer of zeste homolog 2 (EZH2) mRNA, complete cds /cds=(89,2329) /gb=U61145 /gi=1575348 /ug=Hs.77256 /len=2600	37305_at
STK12 (serine/threonine kinase 12)	AF015254	Hs.180655	NM_004217	17p13.1	Cluster Incl. AF015254:Homo sapiens serine/threonine kinase (STK-1) mRNA, complete cds /cds=(58,1101) /gb=AF015254 /gi=4090840	33266_at

						/ug=Hs.180655 /len=1234		
MPB1 (MYC promoter-binding protein 1)	M55914	Hs.284127	NM_005945	1pter-p35	M55914	/FEATURE=	2035_s_at	
						/DEFINITION=HUMCMYCQ Human c-myc binding protein (MBP-1) mRNA, complete cds		
PTTG1 (pituitary tumor-transforming 1)	AA203476	Hs.252587	NM_004219	5q35.1	Cluster Incl. AA203476:zx55e01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446424 /clone_end=5 /gb=AA203476 /gi=1799203 /ug=Hs.159626 /len=828		40412_at	
ICA1 (islet cell autoantigen 1 (69kD))	U38260	Hs.167927	NM_004968	7p22	Cluster Incl. U38260:Human Islet cell autoantigen ICAp69 mRNA, complete cds /cds=(169,942) /gb=U38260 /gi=1675205 /ug=Hs.167927 /len=1415		32634_s_at	
PGD (phosphogluconate dehydrogenase)	U30255	Hs.75888	NM_002631	1p36.3-p36.13	Cluster Incl. U30255:Human phosphogluconate dehydrogenase (hPGDH) gene, complete cds /cds=(6,1457) /gb=U30255 /gi=984324		36963_at	

						/ug=Hs.75888 /len=1536	
FOXM1 (forkhead box M1)	U74612	Hs.239	NM_021953	12p13		Cluster Incl. U74612:Human hepatocyte nuclear factor-3/fork head homolog 11A (HFN-11A) mRNA complete cds /cds=(114,2519) /gb=U74612 /gi=1842252 /ug=Hs.239 /len=3474	34715_at
BPI (bactericidal/permeability-increasing protein)	J04739	Hs.89535	NM_001725	20q11.23-q12		Cluster Incl. J04739:Human bactericidal permeability increasing protein (BPI) mRNA, complete cds /cds=(30,1493) /gb=J04739 /gi=179528 /ug=Hs.89535 /len=1813	37054_at
H2AFY (H2A histone family, member Y)	AF054174	Hs.75258	NM_004893	5q31.3-q32		Cluster Incl. AF054174:Homo sapiens histone macroH2A1.2 mRNA, complete cds /cds=(173,1288) /gb=AF054174 /gi=3341991 /ug=Hs.75258 /len=1881	36576_at
TKT (transketolase (Wernicke-Korsakoff syndrome))	L12711	Hs.89643	NM_001064	3p14.3		Cluster Incl. L12711:Homo sapiens transketolase (tk) mRNA, complete cds	38789_at

syndrome))						/cds=(98,1969) /gb=L12711 /gi=388890 /ug=Hs.89643 /len=2069	1749_at
GCDH (glutaryl-Coenzyme A dehydrogenase)	AD000092	Hs.184141	NM_000159	19p13.2		AD000092 /FEATURE=cds#4 /DEFINITION=CH19HHR23 Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKL, GCDH, CRT, and RAD23A genes, genomic sequence	
RAD54L (RAD54 (S.cerevisiae)-like)	X97795	Hs.66718	NM_003579	1p32		X97795 /FEATURE=cds /DEFINITION=HSRAD54 H.sapiens mRNA homologous to S. cerevisiae RAD54	966_at
GNG5 (guanine nucleotide binding protein (G protein), gamma 5)	AI541042	Hs.5322	NM_005274	1p22		Cluster Incl. AI541042, pec1.2-1.D12.r Homo sapiens cDNA, 5' end /clone_end=5 /gb=AI541042 /gi=4458415 /ug=Hs.5322 /len=688	35272_at
RAB32 (RAB32, member RAS oncogene family)	U59878	Hs.32217	NM_006834	6		Cluster Incl. U59878:Human low-Mr GTP- binding protein (RAB32) mRNA, partial cds	41523_at

						/cds=(0,632) /gb=U59878 /gi=1388196 /ug=Hs.32217 /len=980				
CD63 (CD63 antigen (melanoma 1 antigen))	X62654	Hs.76294	NM_001780	12q12-q13		Cluster Incl. X62654:H.sapiens gene for Me491/CD63 antigen /cds=(69,785) /gb=X62654 /gi=430755 /ug=Hs.76294 /len=873				37003_at
MPO (myeloperoxidase)	M19507	Hs.1817	NM_000250	17q23.1		Cluster Incl. M19507:Human myeloperoxidase mRNA, complete cds /cds=UNKNOWN /gb=M19507 /gi=188657 /ug=Hs.1817 /len=3215				33284_at
TALDO1 (transaldolase 1)	AF010400	Hs.77290	NM_006755	11p15.5-p15.4		Cluster Incl. AF010400:untitled /cds=(50,1063) /gb=AF010400 /gi=2612878 /ug=Hs.77290 /len=1242				37311_at
CDKN3 (cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase))	L25876	Hs.84113	NM_005192	14q22		L25876 /FEATURE= /DEFINITION=HUMPTPB Homo sapiens protein tyrosine phosphatase (CIP2)mRNA, complete cds				1599_at

H2AV(histone H2A.F/Z variant)	AW007731	Hs.301005	NM_012412	7	Cluster Incl. AW007731:w68d11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2512629 /clone_end=3 /gb=AW007731 /gi=5856509 /ug=Hs.9242 /len=659	39092_at
TXN (thioredoxin)	AI653621	Hs.76136	NM_003329	9q31	Cluster Incl. AI653621:t221b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2289213 /clone_end=3 /gb=AI653621 /gi=4737600 /ug=Hs.76136 /len=598	36992_at
ALAS1 (aminolevulinatase, delta-, synthase 1)	Y00451	Hs.78712	NM_000688	3p21.1	Cluster Incl. Y00451:Human mRNA for 5-aminolevulinatase synthase /cds=(83,2011) /gb=Y00451 /gi=36648 /ug=Hs.78712 /len=2156	37674_at
NUCB2 (nucleobindin 2)	X76732	Hs.3164	NM_005013	11p15.1-p14	Cluster Incl. X76732:H.sapiens mRNA for NEFA protein /cds=(219,1481) /gb=X76732 /gi=2708486 /ug=Hs.3164 /len=1586	35643_at
BN51T (BN51 (BHK21) temperature sensitivity complementing)	M17754	Hs.1276	NM_001722	8q21	Cluster Incl. M17754:Human BN51 mRNA, complete cds /cds=(51,1238) /gb=M17754	41694_at

complementing)						/gi=179512 /ug=Hs.1276 /len=1881	
CCR2 (chemokine (C-C motif) receptor 2)	U95626	Hs.395	NM_000647	3p21.1		Cluster Incl. U95626: Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607	37149_s_at
DEFA4 (defensin, alpha 4, corticostatin)	A1250799	Hs.2582	NM_001925	8p23		Cluster Incl. A1250799: q36g07.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-1858620 /clone_end=3 /gb=A1250799 /gi=3847328 /ug=Hs.2582 /len=542	34546_at
HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like))	D16431	Hs.89525	NM_004494	xq25		Cluster Incl. D16431: Human mRNA for hepatoma-derived growth factor, complete cds /cds=(315,1037) /gb=D16431 /gi=598955 /ug=Hs.89525 /len=2376	38779_r_at
EPB72 (erythrocyte membrane protein band 7.2 (stomatin))	X85116	Hs.160483	NM_004099	9q34.1		Cluster Incl. X85116: H. sapiens epb72 gene exon 1 /cds=(61,927) /gb=X85116 /gi=1161561 /ug=Hs.160483 /len=3035	40419_at

						/gi=1161561 /ug=Hs.160483 /len=3035		
DEFA3 (defensin, alpha 3, neutrophil-specific)	L12691	Hs.294176	NM_006217	8pter-p23.3		Cluster Incl. L12691:Human neutrophil peptide-3 gene, complete cds /cds=(50,334) /gb=L12691 /gi=292364 /ug=Hs.178741 /len=452	31508_s_at	
ACTG1 (actin, gamma 1)	X04098	Hs.14376	NM_001614	17q25		Cluster Incl. X04098:Human mRNA for cytoskeletal gamma-actin /cds=(73,1200) /gb=X04098 /gi=28338 /ug=Hs.234733 /len=1918	34160_at	
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	M33197	Hs.169476	NM_002046	12p13		Homo sapiens /REF=M33197 /DEF=Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds /LEN=1268 (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HUNGAPDH/M	
KIAA0008(KIAA0008 gene product)	D13633	Hs.77695	NM_014750	14		Cluster Incl. D13633:Human mRNA for KIAA0008 gene, complete cds /cds=(121,2418) /gb=D13633 /gi=288012	37231_at	

						/ug=Hs.77695 /len=2640			
LDHA (lactate dehydrogenase A)	X02152:	Hs.2795	NM_005566	11p15.4		Cluster Incl. X02152:Human mRNA for lactate dehydrogenase-A (LDH-A, EC 1.1.1.27) /cds=(97,1095) /gb=X02152 /gi=34312 /ug=Hs.2795 /len=1661	41485_at		
ACTN1 (actinin, alpha 1)	M95178	Hs.119000	NM_001102	14q24		Cluster Incl. M95178:Human non-muscle alpha-actinin mRNA, complete cds /cds=(111,2789) /gb=M95178 /gi=178051 /ug=Hs.119000 /len=3081	39330_s_at		
PRG2 (proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic	Z26248	Hs.99962	NM_002728	11q12		Cluster Incl. Z26248:H.sapiens mRNA for eosinophil granule major basic protein /cds=(857,1525) /gb=Z26248 /gi=840510 /ug=Hs.99962 /len=1637	39179_at		
TCN1 (transcobalamin I (vitamin B12 binding protein, R binder family))	J05068	Hs.2012	NM_001062	11q11-q12		Cluster Incl. J05068:human transcobalamin I mRNA, complete cds /cds=(75,1376) /gb=J05068 /gi=307478 /ug=Hs.2012 /len=1537	35919_at		

GGH (gamma-glutamyl hydrolase (conjugase, polygamma-glutamyl hydrolase))	U55206	Hs.78619	NM_003878	: 8p22-q21.13	Cluster Incl. U55206: Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA, complete cds /cds=(59,1015) /gb=U55206 /gi=2957143 /ug=Hs.78619 /len=1265	37263_at
ACTB (actin, beta)	X00351	Hs.288061	NM_001101	7p15-p12	Homo sapiens /REF=X00351 /DEF=Human mRNA -for beta-actin /LEN=1761 /5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	AFFX-HSAC07/X00351
LCN2 (lipocalin 2 (oncogene 24p3))	A1762213	Hs.204238	NM_005564	9q34	Cluster Incl. A1762213: wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=A1762213 /gi=5177880 /ug=Hs.204238 /len=677	32821_at
AGPS (alkylglycerone phosphate synthase)	Y09443	Hs.22580	NM_003659	2q31	Cluster Incl. Y09443: H.sapiens mRNA for alkyl-dihydroxyacetonephosphate synthase precursor /cds=(15,1991) /gb=Y09443 /gi=1922284 /ug=Hs.22580	39225_at

						/len=2074		
H2AFZ (H2A histone family, member Z)	M37583	Hs.119192	NM_002106	4q24	Cluster Incl. M37583:Human histone (H2A.Z) mRNA, complete cds /cds=(106,492) /gb=M37583 /gi=184059 /ug=Hs.119192 /len=873	39337_at		
MGC1780(hypothetical protein MGC1780)	AA926959	Hs.77550	NM_032636	1	Cluster Incl. AA926959:om68h08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1552383 /clone_end=3 /gb=AA926959 /gi=3075856 /ug=Hs.77550 /len=809	37347_at		
CAT (catalase)	AL035079	Hs.76359	NM_001752	11p13	Cluster Incl. AL035079:dJ53C18.1 (Catalase) /cds=(74,1657) /gb=AL035079 /gi=4775614 /ug=Hs.76359 /len=2287	37009_at		
SLC6A7 (solute carrier family 6 (neurotransmitter transporter, L-proline), member 7)	S80071	Hs.241597	NM_014228	5q31-q32	Cluster Incl. S80071:hPROT=brain-specific L-proline transporter [human, hippocampus, mRNA Partial, 1911 nt] /cds=(0,1910) /gb=S80071 /gi=1839289 /ug=Hs.234765 /len=1911	34166_at		

TYMS (thymidylate synthetase)	X02308	Hs.82962	NM_001071	18p11.32	Cluster Incl. X02308:Human mRNA for thymidylate synthase (EC 2.1.1.45) /cds=(105,1046) /gb=X02308 /gi=37478 /ug=Hs.82962 /len=1536	37899_at
C20orf1 (chromosome 20 open reading frame 1)	AB024704	Hs.9329	NM_012112	20q11.2	Cluster Incl. AB024704:Homo sapiens mRNA for fis353, complete cds /cds=(471,2714) - /gb=AB024704 /gi=4589928 /ug=Hs.9329 /len=3403	39109_at
SERPINB1 (serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1)	M93056	Hs.183583	NM_030666	6p25	Cluster Incl. M93056:Human monocyte/neutrophil elastase inhibitor mRNA sequence /cds=UNKNOWN /gb=M93056 /gi=188621 /ug=Hs.183583 /len=1298	33305_at
DEEPEST(mitotic spindle coiled-coil related protein	AF063308	Hs.16244	NM_006461	17	Cluster Incl. AF063308:Homo sapiens coiled-coil related protein DEEPEST (DEEPEST) mRNA, complete cds /cds=(69,3431) /gb=AF063308 /gi=4106355 /ug=Hs.16244 /len=3770	32120_at

SLPI (secretory leukocyte protease inhibitor (antileukoproteainase))	X04470	Hs.251754	NM_003064	20pter-p12.3	Cluster Incl. X04470:Human mRNA for antileukoprotease (ALP) from cervix uterus /cds=(18,416) /gb=X04470 /gi=28638 /lug=Hs.169793 /len=594	32275_at
TTK (TTK protein kinase)	M86699	Hs.169840	NM_003318	6q13-q21	M86699 /FEATURE= /DEFINITION=HUMTTK Human kinase (TTK) mRNA, complete cds	572_at
ANXA1 (annexin A1)	X05908	Hs.78225	NM_000700	9q12-q21.2	Cluster Incl. X05908:Human mRNA for lipocortin /cds=(74,1114) /gb=X05908 /gi=34387 /lug=Hs.78225 /len=1399	37403_at
CTSG (cathepsin G)	M16117	Hs.100764	NM_001911	14q11.2	Cluster Incl. M16117:Human cathepsin G mRNA, complete cds /cds=(8,775) /gb=M16117 /gi=181181 /lug=Hs.100764 /len=857	37105_at
MS4A3 (membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell- specific))	L35848	Hs.99960	NM_006138	11q12-q13.1	Cluster Incl. :Homo sapiens IgE receptor beta chain (HTm4) mRNA, complete cds /cds=UNKNOWN /gb=L35848 /gi=561638 /lug=Hs.99960 /len=1646	32451_at

						/ug=Hs.99960 /len=1646	
MGST2 (microsomal glutathione S-transferase 2)	U77604	Hs.81874	NM_002413	4q28-q31	U77604	/FEATURE= 820_at /DEFINITION=HSU77604 Homo sapiens microsomal glutathione S-transferase 2 (MGST2) mRNA, complete cds	
CLC (Charot-Leyden crystal protein)	L01664	Hs.132004	NM_013246	11q13.3	Cluster Incl. L01664:Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds /cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586	36809_at	
FLJ10140(hypothetical protein FLJ10140)	AL031588	Hs.250671	NM_018006	22	Cluster Incl. AL031588:dJ1163J1.3 (novel protein similar to mouse B99) /cds=(0,2140) /gb=AL031588 /gi=4007108 /ug=Hs.122552 /len=2821	39872_at	
GADD45A (growth arrest and DNA-damage-inducible, alpha)	M60974	Hs.80409	NM_001924	1p31.2-p31.1	M60974	/FEATURE= 1911_s_at /DEFINITION=HUMGADD45 Human growth arrest and DNA-damage-inducible	

						protein (gadd45) mRNA, complete cds	
OAT (ornithine aminotransferase (gyrate atrophy))	M12267	Hs.75485	NM_000274	10q26		Cluster Incl. M12267:Human ornithine aminotransferase mRNA, complete cds /cds=(54,1373) /gb=M12267 /gi=189328 /ug=Hs.75485 /len=2013	36636_at
CEACAM8 (carcinoembryonic antigen-related cell adhesion molecule 8)	M33326	Hs.41	NM_001816	19q13.2		Cluster Incl. M33326:Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds /cds=(86,1135) /gb=M33326 /gi=189101 /ug=Hs.41 /len=2287	33530_at
S100A8 (S100 calcium-binding protein A8 (calgranulin A))	A1126134	Hs.100000	NM_002984	1q21		Cluster Incl. A1126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 /gb=A1126134 /gi=3594648 /ug=Hs.100000 /len=446	41096_at
U67369	U67369	Hs.73172	NM_005263	1p22		Cluster Incl. U67369:Human growth factor independence-1 (Gfi-1) mRNA, complete cds /cds=(267,1535) /gb=U67369 /gi=1698691 /ug=Hs.73172 /len=2799	33977_at

TFDP2 (transcription factor Dp-2 (E2F dimerization partner 2))	L40386	Hs.19131	NM_006286	3q23	L40386 /FEATURE=mRNA /DEFINITION=HUMDP2M Human DP-2 mRNA, complete cds	633_s_at
ELA2 (elastase 2, neutrophil)	M34379	Hs.99863	NM_001972	19p13.3	Cluster Incl. M34379:Human elastase/medullasin mRNA, complete cds /cds=(38,841) /gb=M34379 /gi=187116 /ug=Hs.99863 /len=920 -	37096_at
ITGAM (Integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170),	J03925	Hs.172631	NM_000632	16p11.2	Cluster Incl. J03925:Human Mac-1 gene encoding complement receptor type 3, CD11b, complete cds /cds=(72,3533) /gb=J03925 /gi=187284 /ug=Hs.172631 /len=4699	38533_s_at
AZU1 (azurocidin 1 (cationic antimicrobial protein 37))	M96326	Hs.72885	NM_001700	19p13.3	Cluster Incl. M96326:Human azurocidin gene, complete cds /cds=(16,771) /gb=M96326 /gi=179301 /ug=Hs.72885 /len=913	33963_at

PKM2 (pyruvate kinase, muscle)	M26252	Hs.198281	NM_002654	15q22	Cluster Incl. M26252:Human TCB gene encoding cytosolic thyroid hormone-binding protein, complete cds /cds=(89,1684) /gb=M26252 /gi=338826 /ug=Hs.198281 /len=2308	32378_at
S100A9 (S100 calcium-binding protein A9 (calgranulin B))	W72424	Hs.112405	NM_002965	1q21	Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345592 /clone_end=3 /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604	41471_at
CKS2 (CDC28 protein kinase 2)	X54942	Hs.83758	NM_001827	9q22	Cluster Incl. X54942:H.sapiens cks2 mRNA for Cks1 protein homologue /cds=(95,334) /gb=X54942 /gi=29978 /ug=Hs.83758 /len=612	40690_at
GAPD (glyceraldehyde-3-phosphate dehydrogenase)	U34995	Hs.169476	NM_002046	12p13	Cluster Incl. U34995:Human normal keratinocyte subtraction library mRNA, clone H22a, complete sequence /cds=UNKNOWN /gb=U34995 /gi=1497857 /ug=Hs.195188 /len=1626	35905_s_at

LOC95295(hypothetical gene supported by V00599; BC001938; BC007605; BC008791	V00599				6	V00599 /DEFINITION=HSTUB2 Human mRNA fragment encoding beta-tubulin. (from clone D-beta-1)	151_s_at
ADAM15 (a disintegrin and metalloproteinase domain 15 (metargidin))	U41767	Hs.92208	NM_003815	1q21.3		Cluster Incl. U41767:Human metargidin precursor mRNA, complete cds /cds=(7,2451) /gb=U41767 /gj=1235673 /ug=Hs.92208 /len=2725	38282_at
LOC51304(DHHC1 protein)	AF052182	Hs.14896	NM_016598	3		Cluster Incl. AF052182:Homo sapiens clone 24590 mRNA sequence /cds=UNKNOWN /gb=AF052182 /gj=3360494 /ug=Hs.14896 /len=1298	39751_at
RAB13 (RAB13, member RAS oncogene family)	X75593	Hs.151536	NM_002870	12q13		Cluster Incl. X75593:H.sapiens mRNA for rab 13 /cds=(139,750) /gb=X75593 /gj=452319 /ug=Hs.151536 /len=1238	40210_at
BZRP (benzodiazepine receptor (peripheral))	M36035	Hs.202	NM_000714	22q13.31		Cluster Incl. M36035:Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds /cds=(61,570) /gb=M36035	32806_at

						/gi=184333 /ug=Hs.202 /len=811	
KNXL6 (kinesin-like 6 (mitotic centromere-associated kinesin))	U63743	Hs.69360	NM_006845	1		Cluster Incl. U63743:Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds /cds=(54,2231) /gb=U63743 /gi=1695881 /ug=Hs.69360 /len=2740	36837_at
MTX1 (metaxin 1)	U46920	Hs.247551	NM_002455	1q21		Cluster Incl. U46920:Human metaxin (MTX) gene, complete cds /cds=(0,953) /gb=U46920 /gi=1326107 /ug=Hs.181246 /len=1065	40890_at
DOK1 (docking protein 1, 62kD (downstream of tyrosine kinase 1)	U70987	Hs.103854	NM_001381	2p13		U70987 /FEATURE= /DEFINITION=HSU70987 Human GAP binding protein p62dok (DOK) mRNA, complete cds	816_g_at
E2-EPF(ubiquitin carrier protein)	M91670			17		M91670 /FEATURE= /DEFINITION=HUME2EPI Human ubiquitin carrier protein (E2-EPF) mRNA, complete cds	893_at

NCF4 (neutrophil cytosolic factor 4 (40kD))	AL008637	Hs.196352	NM_000631	22q13.1	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 - /gi=3136000 /lug=Hs.196352 /len=1744	38894_g_at
PGK1 (phosphoglycerate kinase 1)	V00572	Hs.78771	NM_000291	xq13	Cluster Incl. V00572:Human mRNA encoding phosphoglycerate kinase /cds=(79,1332) /gb=V00572 /gi=35434 /lug=Hs.78771 /len=1767	37677_at
S100P (S100 calcium-binding protein P)	AA131149	Hs.2962	NM_005980	4p16	Cluster Incl. AA131149:zo16d05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-587049 /clone_end=5 /gb=AA131149 /gi=1692640 /lug=Hs.2962 /len=464	34319_at

NKG7 (natural killer cell group 7 sequence)	S69115	Hs.10306	NM_005601	19q13.4	Cluster Incl. S69115:granulocyte colony-stimulating factor induced gene [human, CML patient, bone marrow mononuclear cells, mRNA, 833 nt] /cds=(180,677) /gb=S69115 /gi=545708 /ug=Hs.10306 /len=833	37121_at
ITGA5 (integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	X06256	Hs.149609	NM_002265	12q11-q13	Cluster Incl. X06256:Human mRNA for integrin alpha 5 subunit /cds=(23,3172) /gb=X06256 /gi=31437 /ug=Hs.149609 /len=4204	39753_at
PKMYT1(membrane-associated tyrosine-and threonine-specific cdc2-inhibitory kinase	U56816	Hs.77783	NM_004203	16	U56816 /FEATURE= /DEFINITION=HSU56816 Human kinase Myt1 (Myt1) mRNA, complete cds	480_at
CEACAM6 (carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross	M18728	Hs.73848	NM_002483	19q13.2	Cluster Incl. M18728:Human nonspecific crossreading antigen mRNA, complete cds /cds=UNKNOWN /gb=M18728 /gi=189084 /ug=Hs.73848 /len=2533	36105_at

CREG (cellular repressor of E1A-stimulated genes)	AF084523	Hs.5710	NM_003851	1q24	Cluster Incl. AF084523:Homo sapiens cellular repressor of E1A-stimulated genes CREG mRNA, complete cds /cds=(33,695) /gb=AF084523 /gi=3550342 /ug=Hs.5710 /len=1974	35311_at
KIAA0374(syntrophin)	AB002372			20	Cluster Incl. AB002372:Human mRNA for KIAA0374 gene, complete cds /cds=(642,2258) /gb=AB002372 /gi=2224688 /ug=Hs.100837 /len=5530	41107_at
MMP9 (matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase	J05070	Hs.151738	NM_004994	20q11.2-q13.1	Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334	31859_at
CDW52 (CDW52 antigen (CAMPATH-1 antigen))	N90866	Hs.276770	NM_001803	1p36	Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-301723 /clone_end=3 /gb=N90866 /gi=1444193 /ug=Hs.214742 /len=577	34210_at

TRB@ (T cell receptor beta locus)	M12886	Hs.303157		7q35	M12886 /DEFINITION=HUMTCBY Human T-cell receptor active beta-chain mRNA, complete cds	1105_s_at
TAB2(TAK1-binding protein 2)	AB018276	Hs.109727	NM_015093		Cluster Incl. AB018276:Homo sapiens mRNA for KIAA0733 protein, partial cds /cds=(0,1586) /gb=AB018276 /gi=3882186 /ug=Hs.109727 /len=3479	38980_at
TNFRSF7 (tumor necrosis factor receptor superfamily, member 7)	M63928	Hs.180841	NM_001242	12p13	Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204	38578_at
KIAA0275(KIAA0275 gene product)	D87465	Hs.74583	NM_014767		Cluster Incl. D87465:Human mRNA for KIAA0275 gene, complete cds /cds=(316,1590) /gb=D87465 /gi=1665814 /ug=Hs.74583 /len=5316	36155_at
PTCH (patched (Drosophila) homolog)	U59464	Hs.159526	NM_000264	9q22.3	Cluster Incl. U59464:Human PATCHED protein (PTC) mRNA, complete cds	38214_at

						/cds=(0,4343) /gb=U59464 /gi=1381235 /ug=Hs.159526 /len=4344					
TRAM(translocating chain-associating membrane protein)	X63679	Hs.4147	NM_014294			Cluster Incl. X63679:H.sapiens mRNA for TRAMP protein /cds=(121,1245) /gb=X63679 /gi=37264 /ug=Hs.4147 /len=1267					34796_at
HLA-DMA (major histocompatibility complex, class II, DM alpha)	X62744	Hs.77522	NM_006120		6p21.3	Cluster Incl. X62744:Human RING6 mRNA for HLA class II alpha chain-like product /cds=(45,830) /gb=X62744 /gi=36062 /ug=Hs.77522 /len=1079					37344_at
HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1)	X00457	Hs.914			6p21.3	Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048					38833_at
KIAA1128(KIAA1128 protein)	U90912	Hs.81897				Cluster Incl. U90912:Human clone 23865 mRNA sequence /cds=UNKNOWN /gb=U90912 /gi=1913892 /ug=Hs.81897					37617_at

						/len=1633				41723_s_at
HLA-DRB1 (major histocompatibility complex, class II, DR beta 1)	M32578	Hs.180255	NM_002124	6p21.3		Cluster Incl. M32578:Human MHC class II HLA-DR beta-1 mRNA (DR2.3), 5end /cds=(61,861) /gb=M32578 /gi=188305 /ug=Hs.181366 /len=1216				
MMD (monocyte to macrophage differentiation-associated)	X85750	Hs.79889	NM_012329	17q		Cluster Incl. X85750:H.sapiens mRNA for transcript associated with monocyte to macrophage differentiation /cds=(81,797) /gb=X85750 /gi=1006664 /ug=Hs.79889 /len=2518				37565_at
HLA-DMB (major histocompatibility complex, class II, DM beta)	U15085	Hs.1162	NM_002118	6p21.3		Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162 /len=1362				41609_at
TGFB3 (transforming growth factor, beta receptor III (betaglycan, 300kD))	L07594	Hs.79059	NM_003243	1p33-p32		L07594 /DEFINITION=HUMTGF3C transforming growth factor-beta type III /FEATURE= Human				1897_at

						receptor (TGF-beta) mRNA, complete cds	
KRT10 (keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris))	X14487	Hs.99936	NM_000421	17q21-q23		Cluster Incl. X14487:Human gene for acidic (type I) cytokeratin 10 /cds=(25,1806) /gb=X14487. /gi=26316 /ug=Hs.99936 /len=2166	38610_s_at
MSF (MLL septin-like fusion (NOTE: non-standard symbol and name))	AB023208	Hs.181002	NM_006640	17q25		Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	41220_at
	A1700633					Cluster Incl. A1700633:we38g03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2343412 /clone_end=3 /gb=A1700633 /gi=4988533 /ug=Hs.4815 /len=565	34840_at
CASP7 (caspase 7, apoptosis-related cysteine protease)	U67319	Hs.9216	NM_001227	10q25		Cluster Incl. U67319:Human Lice2 beta cysteine protease mRNA, complete cds /cds=(228,1238) /gb=U67319 /gi=1894912 /ug=Hs.9216 /len=2602	38281_at

SNRPN (small nuclear ribonucleoprotein polypeptide N)	U41303	Hs.48375	NM_003097	15q12	Cluster Incl. U41303:Human small nuclear ribonucleoprotein particle N (SNRPN) mRNA, complete cds /cds=(465,1187) /gb=U41303 /gi=1145774 /ug=Hs.48375 /len=1326	34B42_at
HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501	38095_i_at
NCOA1 (nuclear receptor coactivator 1)	AJ000882	Hs.74002	NM_003743	2p23	Cluster Incl. AJ000882:Homo sapiens mRNA for steroid receptor coactivator 1e /cds=(201,4400) /gb=AJ000882 /gi=2924310 /ug=Hs.74002 /len=4709	36118_at
HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814	38096_f_at

					/len=1501	
PSCD1 (pleckstrin homology, Sec7 and coiled/coil domains 1(cytchesin 1))	M85169	Hs.1050	NM_004762	17q25	Cluster Incl. M85169:Human homologue of yeast sec7 mRNA, complete cds /cds=(69,1265) /gb=M85169 /gi=338001 /ug=Hs.1050 /len=3301	38666_at
KIAA1041(KIAA1041 protein)	AB028964	Hs.26023	NM_014947		Cluster Incl. AB028964:Homo sapiens mRNA for KIAA1041 protein, complete cds /cds=(312,2180) /gb=AB028964 /gi=5689418 /ug=Hs.26023 /len=5341	35163_at
SLC7A6 (solute carrier family 7 (cationic amino acid transporter, y+ system), member 6)	D87432	Hs.10315	NM_003983	16q22.1-q22.3	Cluster Incl. D87432:Human mRNA for KIAA0245 gene, complete cds /cds=(261,1808) /gb=D87432 /gi=1665758 /ug=Hs.10315 /len=6296	39533_at
	AF038199				Cluster Incl. AF038199:Homo sapiens clone 23728 mRNA sequence /cds=UNKNOWN /gb=AF038199	38154_at

						/gi=2795920 /ug=Hs.153106 /len=1112			
UCP2 (uncoupling protein 2 (mitochondrial, proton carrier))	U94592	Hs.80658	NM_003355	11q13		Cluster Incl. U94592:Human uncoupling protein homolog (UCPH) mRNA, complete cds /cds=(314,1243) /gb=U94592 /gi=2052354 /ug=Hs.80658 /len=1888	37591_at		
HLA-DQB1 (major histocompatibility complex, class II, DQ beta 1)	M81141	Hs.73931	NM_002123	6p21.3		Cluster Incl. M81141:Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), complete cds /cds=(35,820) /gb=M81141 /gi=188202 /ug=Hs.73933 /len=1171	36773_f_at		
NCOA1 (nuclear receptor coactivator 1)	U59302	Hs.74002	NM_003743	2p23		U59302 /FEATURE= /DEFINITION=HSU59302 Human steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds	484_at		
KIAA0542(KIAA0542 gene product)	AB011114	Hs.62209				Cluster Incl. AB011114:Homo sapiens mRNA for KIAA0542 protein, complete cds /cds=(393,3299) /gb=AB011114 /gi=3043607 /ug=Hs.62209 /len=5280	36545_s_at		

JAK1 (Janus kinase 1 (a protein tyrosine kinase))	AL039831	Hs.50651	NM_002227	1p32.3-p31.3	Cluster AL039831:DKFZp434D1112_s1 sapiens cDNA, 3 end /clone=DKFZp434D1112 /clone_end=3 /gb=AL039831 /gi=5866713 /ug=Hs.50651 /len=579	Incl. 34877_at
IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41164_at
DKFZP434C171(DKFZP434C171 protein	AL080169	Hs.209100	NM_015621		Cluster Incl. AL080169:Homo sapiens mRNA; cDNA DKFZp434C171 (from clone DKFZp434C171) /cds=(0,544) /gb=AL080169 /gi=5262637 /ug=Hs.209100 /len=2595	34183_at
	X6730				Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407	41165_g_at

						/ug=Hs.179543 /len=1453	
TMSB10 (thymosin, beta 10)	M92383	Hs.76293	NM_021103	2		Cluster Incl. M92383:Homo sapiens thymosin beta-10 gene, 3end /cds=(0,149) /gb=M92383 /gi=339696 /ug=Hs.169250 /len=400	31481_s_at
AHNAK (AHNAK nucleoprotein (desmoyokin))	M80899	Hs.301417		11q12-q13		Cluster Incl. M80899:Human novel protein AHNAK mRNA, partial sequence /cds=(0,3835) /gb=M80899 /gi=178282 /ug=Hs.76549 /len=4051	37027_at
KIAA1002(KIAA1002 protein)	AB023219	Hs.20340				Cluster Incl. AB023219:Homo sapiens mRNA for KIAA1002 protein, complete cds /cds=(800,3322) /gb=AB023219 /gi=4589647 /ug=Hs.102483 /len=4331	41366_at
HBOA(histone acetyltransferase)	AI951946	Hs.21907	NM_007067			Cluster Incl. AI951946:wx39f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2546059 /clone_end=3 /gb=AI951946 /gi=5744256 /ug=Hs.244 /len=523	41338_at

RNF6 (ring finger protein (C3H2C3 type 6)	AJ010346	Hs.32597	NM_005977	13q12.2	Cluster Incl. AJ010346:Homo sapiens mRNA for RING-H2 protein RNF6, alternative exon 1a /cds=(360,2417) /gb=AJ010346 /gi=4583651 /ug=Hs.32597 /len=3503	35656_at
IGHM (immunoglobulin heavy constant mu)	X58529	Hs.302063		14q32.33	Cluster Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN /gb=X58529 /gi=33480 /ug=Hs.179543 /len=2325	41166_at
KIAA0660(ras-GTPase-activating protein (GAP<120>) SH3-domain-binding protein 2)	AB014560	Hs.6727	NM_012297		Cluster Incl. AB014560:Homo sapiens mRNA for KIAA0660 protein, complete cds /cds=(120,1568) /gb=AB014560 /gi=3327133 /ug=Hs.6727 /len=4210	35793_at
KIAA1093(KIAA1093 protein)	AB029016	Hs.117333			Cluster Incl. AB029016:Homo sapiens mRNA for KIAA1093 protein, partial cds /cds=(0,3613) /gb=AB029016 /gi=5689522 /ug=Hs.117333 /len=4159	37487_at

PRKRIR (protein-kinase, interferon-inducible double stranded RNA dependent inhibitor,	AL049970	Hs.177574	NM_004705	11q13.5	Cluster Incl. AL049970:Homo sapiens mRNA; cDNA DKFZp564B102 (from clone DKFZp564B102) /cds=(0,965) /gb=AL049970 /gi=4884219 /ug=Hs.177574 /len=2724	41141_at
SCAP1 (src family associated phosphoprotein 1)	Y11215	Hs.19126	NM_003726	17q21.3	Cluster Incl. Y11215:Homo sapiens mRNA for SKAP55 protein /cds=(70,1149) /gb=Y11215 /gi=2252495 /ug=Hs.19126 /len=1524	38862_at
FLJ10140(hypothetical protein FLJ10140)	AL031588	Hs.250671	NM_018006		Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438	41660_at
UBE2D2 (ubiquitin-conjugating enzyme E2D 2 (homologous to yeast UBC4/5))	A1310002	Hs.108332	NM_003339	5p14.2-q23.3	Cluster Incl. A1310002:qp77c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1914548 /clone_end=3 /gb=A1310002	38705_at

						/gi=4004873 /ug=Hs.108332 /len=656	
KIAA0226(KIAA0226 gene product)	D86979	Hs.141296				Cluster Incl. D86979:Human mRNA for KIAA0226 gene, complete cds /cds=(622,2877) /gb=D86979 /gi=1504031 /ug=Hs.141296 /len=5891	31802_at
SEP2(sepin 6)	D50918	Hs.90998			Hs.90998	Cluster Incl. D50918:Human mRNA for KIAA0128 gene, partial cds /cds=(0,1276) /gb=D50918 /gi=1469178 /ug=Hs.90998 /len=4612	38826_at
UBE2N (ubiquitin-conjugating enzyme E2N (homologous to yeast UBC	D83004	Hs.75355			NM_003348	12 Cluster Incl. D83004:Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds /cds=(63,521) /gb=D83004 /gi=1181557 /ug=Hs.75355 /len=1203	36604_at
PKD2 (polycystic kidney disease 2 (autosomal dominant))	AL050147	Hs.91146			NM_016457	19q13.2 Cluster Incl. AL050147:Homo sapiens mRNA; cDNA DKFZp586E0820 (from clone DKFZp586E0820) /cds=(0,1630)	38269_at

						/gb=AL050147 /gi=4884153 /ug=Hs.91146 /len=1837				
RUNX3 (runt-related transcription factor 3)	Z35278	Hs.170019	NM_004350	1p36	Z35278	/FEATURE=mRNA /DEFINITION=HSAML1RN H.sapiens PEBP2aC1 acute myeloid leukaemia mRNA	106_at			
RAGA(Ras-related GTP-binding protein)	U41654	Hs.57304	NM_006570		Cluster Incl. U41654;Human adenovirus protein E3-14.7k interacting protein 1 (FIP- 1) mRNA, complete cds /cds=(243,1184) /gb=U41654 /gi=2058395 /ug=Hs.57304 /len=1610		35316_at			
PPP1CC (protein phosphatase 1, catalytic subunit, gamma isoform)	X74008	Hs.79081	NM_002710	12q24.1-q24.2	Homo sapiens /DEF=Cluster Incl. :H.sapiens mRNA for protein phosphatase 1 gamma /cds=(154,1125) /gb= /gi=402777 /ug=Hs.79081 /len=2263 /LEN=2431		37725_at			
H2BFL (H2B histone family, member L)	AI688098	Hs.239884	NM_003526	6p21.3	Cluster Incl. AI688098;wc92f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-		33458_r_at			

						2326119 /clone_end=3 /gb=AI688098 /gi=4899392 /ug=Hs.239884 /len=576	
BIN1 (bridging integrator 1)	U68485	Hs.193163	NM_004305	2q14	U68485 /FEATURE=459_s_at /DEFINITION=HSU68485 Homo sapiens bridging integrator protein-1 (BIN1) mRNA, complete cds		
	AI749193				Cluster Ind. AI749193:at40a04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE- 2374494 /clone_end=3 /gb=AI749193 /gi=5127457 /ug=Hs.17639 /len=544	40623_at	
KIAA0911(calsyntenin 1)	AB020718	Hs.29665	NM_014944		Cluster Ind. AB020718:Homo sapiens mRNA for KIAA0911 protein, complete cds /cds=(793,3738) /gb=AB020718 /gi=4240310 /ug=Hs.29665 /len=5219	41498_at	
	M13560				Cluster Ind. M13560:Human la-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518	35016_at	

						/ug=Hs.84298 /len=2080	
REPER (arginine-glutamic acid dipeptide (RE) repeats)	AB007927	Hs.194369	NM_012102	1p36.1-p36.2		Cluster Incl. AB007927:Homo sapiens mRNA for KIAA0458 protein, complete cds /cds=(155,3961) /gb=AB007927 /gi=3413877 /ug=Hs.194369 /len=6642	32253_at
NIFU(nitrogen fixation cluster-like)	U47101	Hs.9908				Cluster Incl. U47101:Human NifU-like protein (hNifU) mRNA, partial cds /cds=(0,366) /gb=U47101 /gi=1685101 /ug=Hs.9908 /len=819	39165_at
CD48 (CD48 antigen (B-cell membrane protein))	M37766	Hs.901	NM_001778	1q21.3-q22		Cluster Incl. M37766:Human MEM-102 glycoprotein mRNA, complete cds /cds=(20,751) /gb=M37766 /gi=187518 /ug=Hs.901 /len=1058	38006_at
BIN1 (bridging integrator 1)	AF001383	Hs.193163	NM_004305	2q14		Cluster Incl. AF001383:Homo sapiens amphiphysin II mRNA, complete cds /cds=(171,1619) /gb=AF001383 /gi=2199534 /ug=Hs.193163 /len=2115	32238_at

KIAA0239(KIAA0239 protein)	D87076	Hs.9729	NM_015288		Cluster Incl. D87076:Human mRNA for KIAA0239 gene, partial cds /cds=(0,1716) /gb=D87076 /gi=1510152 /ug=Hs.9729 /len=5630	38342_at
CSK (c-src tyrosine kinase)	X59932	Hs.77793	NM_004383	15q23-q25	X59932 /FEATURE=mRNA /DEFINITION=HSCSRCKIN Human mRNA for C-SRC-kinase -	1768_s_at
RGS10 (regulator of G-protein signalling 10)	AF045229	Hs.82280	NM_002925	10q25	Cluster Incl. AF045229:Homo sapiens regulator of G protein signalling 10 mRNA, complete cds /cds=(132,635) /gb=AF045229 /gi=2906029 /ug=Hs.82280 /len=753	33121_g_at
RBL2 (retinoblastoma-like 2 (p130))	X76061	Hs.79362	NM_005611	16q12.2	Cluster Incl. X76061:H.sapiens p130 mRNA for 130K protein /cds=(69,3488) /gb=X76061 /gi=416030 /ug=Hs.79362 /len=4835	32597_at
ZFR(zinc finger RNA binding protein)	A1743507	Hs.173518	NM_016107		Cluster Incl. A1743507:w72a06.x2 Homo sapiens cDNA, 3 end /clone=IMAGE-	40610_at

						2361106 /clone_end=3 /gb=A1743507 /gi=5111795 /ug=Hs.173518 /len=733	
SIT(SHP2 interacting transmembrane adaptor	AJ010059	Hs.88012	NM_014450			Cluster Incl. AJ010059:Homo sapiens SIT protein /cds=(87,677) /gb=AJ010059 /gi=4688891 /ug=Hs.88012 /len=1232	40723_at
PFTK1 (PFTAIRE protein kinase 1	AB020641	Hs.57856	NM_012395	7q21-q22		Cluster Incl. AB020641:Homo sapiens mRNA for KIAA0834 protein, complete cds /cds=(144,1499) /gb=AB020641 /gi=4240156 /ug=Hs.57856 /len=4957	36502_at
CDR2 (cerebellar degeneration-related protein (62kD))	M63256	Hs.75124		16p12.3		Cluster Incl. M63256:Human major Yo paraneoplastic antigen (CDR2) mRNA, 3 end /cds=(0,1529) /gb=M63256 /gi=180186 /ug=Hs.75124 /len=2570	36190_at
IFI16 (interferon, gamma-inducible protein 16)	M63838	Hs.155530	NM_005531	1q22		M63838 /FEATURE= /DEFINITION=HUMIF16A Human interferon-gamma induced protein (IFI 16) gene, complete cds	1456_s_at

TCL1A (T-cell leukemia/lymphoma 1A)	X82240	Hs.2484	NM_021966	14q32.1	Cluster Incl. X82240:H.sapiens mRNA for Tcell leukemia/lymphoma 1 /cds=(45,389) /gb=X82240 /gi=624960 /ug=Hs.2484 /len=1312	39318_at
NAF1(Nef-associated factor 1	AJ011896	Hs.109281	NM_006058		Cluster Incl. AJ011896: Homo sapiens mRNA for HIV-1, Nef-associated factor 1 beta (Naf1 beta) /cds=(110,2017) /gb=AJ011896 /gi=3758820 /ug=Hs.109281 /len=2710	38970_s_at
CD37 (CD37 antigen)	X14046	Hs.153053	NM_001774	19p13-q13.4	Cluster Incl. X14046: Human mRNA for leukocyte antigen CD37 /cds=(63,908) /gb=X14046 /gi=29793 /ug=Hs.153053 /len=1125	31670_at
PLCG1 (phospholipase C, gamma 1 (formerly subtype 148	AL022394	Hs.268177	NM_002660	20q12-q13.1	Cluster Incl. AL022394:dJ511B24.2 (1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 /cds=(68,3940) /gb=AL022394 /gi=3288442 /ug=Hs.317	34351_at

						/len=5151	
					AB018272	Cluster Incl. AB018272:Homo sapiens mRNA for KIAA0729 protein, partial cds /cds=(0,3591) /gb=AB018272 /gi=3882178 /ug=Hs.180948 /len=4143	41218_at
BLK (B lymphoid tyrosine kinase)				Hs.2243	S76617	S76617 /FEATURE= /DEFINITION=S76617 blk=protein tyrosine kinase [human, B lymphocytes, mRNA, 2608 nt]	854_at
					H24861	Cluster Incl. H24861:yl42e11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-160940 /clone_end=5 /gb=H24861 /gi=893760 /ug=Hs.90145 /len=517	33168_at
NFATC1 (nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1)				Hs.96149	U08015	Cluster Incl. U08015:Human NF-A1c mRNA, complete cds /cds=(239,2389) /gb=U08015 /gi=500631 /ug=Hs.96149	39143_at

						/len=2743	
						Transcription Factor Oct-1a/1b, Alt. Splice 2, Oct-1b	1171_s_at
IFNAR2 (Interferon (alpha, beta and omega) receptor 2)	L42243	Hs.86958	NM_000874	21q22.11	L42243	/FEATURE=cds#3 /DEFINITION=HUMIFNAM08 Homo sapiens (clone 51H8) alternatively spliced interferon receptor (IFNAR2) gene, exon 9 and complete cds s	1568_s_at
CD79A (CD79A antigen (immunoglobulin-associated alpha))	U05259	Hs.79630	NM_001783	19q13.2	Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=U05259 /gi=452561 /ug=Hs.79630 /len=1107		38017_at
XPA (xeroderma pigmentosum, complementation group A)	D14533	Hs.192803	NM_000380	9q22.3	D14533	/FEATURE= /DEFINITION=HUMXPAC Human mRNA for XPAC protein	1307_at
TLK1 (tousled-like kinase 1)	D50927	Hs.18895	NM_012290	8p22-p12	Cluster Incl. D50927:Human mRNA for KIAA0137 gene, complete cds /cds=(1088,2737) /gb=D50927		32219_at

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						/gi=1489196 /ug=Hs.18895 /len=4454	
SSH3BP1 (spectrin SH3 domain binding protein 1)	AF001628	Hs.24752	NM_005470	10p11.2		Cluster Incl. AF001628:Homo sapiens interactor protein AbiBP4 (AbiBP4) mRNA, complete cds /cds=(48,1403) /gb=AF001628 /gi=4100618 /ug=Hs.204036 /len=2175	38924_s_at
KIAA0494(KIAA0494 gene product)	AB007963	Hs.62515	NM_014774			Cluster Incl. AB007963:Homo sapiens mRNA for KIAA0494 protein, complete cds /cds=(977,2464) /gb=AB007963 /gi=3413937 /ug=Hs.62515 /len=5766	41830_at
KIAA0014(KIAA0014 gene product)	D25216	Hs.155650	NM_014665			Cluster Incl. D25216:Human mRNA for KIAA0014 gene, complete cds /cds=(146,1627) /gb=D25216 /gi=434774 /ug=Hs.155650 /len=5323	32062_at
	U92980					Cluster Incl. U92980:Homo sapiens clone DT1P1A10 mRNA, CAG repeat region /cds=UNKNOWN /gb=U92980	33242_at

						/gi=2781388 /ug=Hs.178207 /len=1423	
CD19 (CD19 antigen)	M28170	Hs.96023	NM_001770	16p11.2	M28170	/DEFINITION=HUMCSPC Human cell surface protein CD19 (CD19) gene, complete cds	1096_g_at
M17S2 (membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen	D30756	Hs.277721	NM_005699	17q21.1	Cluster Incl. D30756:Human mRNA for KIAA0049 gene, complete cds /cds=(140,3040) /gb=D30756 /gi=488500 /ug=Hs.233745 /len=4654		33444_at
LRMP (lymphoid-restricted membrane protein)	U10485	Hs.40202	NM_006152	12p12	Cluster Incl. U10485:Human lymphoid-restricted membrane protein (Jaw1) mRNA, complete cds /cds=(574,2241) /gb=U10485 /gi=505685 /ug=Hs.40202 /len=2417		35974_at
FLJ20274(hypothetical protein FLJ20274)	AA442799	Hs.268371	NM_017736		Cluster Incl. AA442799:zv69b10.r1 Homo sapiens cDNA, 5' end /clone=IMAGE-758875 /clone_end=5 /gb=AA442799		40868_at

						/gi=2155474 /ug=Hs.173992 /len=512	
IL10RA (interleukin 10 receptor, alpha)	U00672	Hs.327	NM_001558	11q23		Cluster Incl. C:Human interleukin-10 receptor mRNA, complete cds /cds=(61,1797) /gb=U00672 /gi=482802 /ug=Hs.327 /len=3632	35659_at
RNF4 (ring finger protein 4)	AB000468	Hs.66394	NM_002938	4p16.3		Cluster Incl. AB000468:Homo sapiens mRNA for zinc finger protein, complete cds, clone-RES4-26 /cds=(297,869) /gb=AB000468 /gi=1843400 /ug=Hs.66394 /len=2903	35777_at
FCGR2B (Fc fragment of IgG, low affinity IIb, receptor for (CD32))	M28696	Hs.278443	NM_004001	1q23		Cluster Incl. M28696:Human low-affinity IgG Fc receptor (beta-Fc-gamma-RII) mRNA, complete cds /cds=(41,916) /gb=M28696 /gi=184843 /ug=Hs.233450 /len=1416	34663_at
CLPTM1 (cleft lip and palate associated transmembrane protein	AF037339	Hs.106671	NM_001294	19q13.2-q13.3		Cluster Incl. AF037339:Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds	41413_at

					/cds=(15,2024) /gb=AF037339 /gi=4063032 /ug=Hs.106671 /len=2468	
SP140(nuclear body protein Sp140)	U36500	Hs.309943	NM_007237		Cluster Incl. U36500:Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds /cds=(116,2764) /gb=U36500 /gi=1173663 /ug=Hs.85283 /len=3252	40700_at

Table 13:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description UniGene Build #95	Gene Name
MYH11 (myosin, heavy polypeptide 11, smooth muscle)	AF001548	Hs.78344	NM_002474	16p13.13-p13.12	AF001548 /FEATURE=mRNA /DEFINITION=HUA001548 Human Chromosome 16 BAC clone C17987SK-A- 815A9, complete sequence	767_at
ARHGAP4 (Rho GTPase activating protein 4)	X78817	Hs.3109	NM_001666	xq28	Cluster Incl. X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817 /gl=840785 /ug=Hs.3109 /len=3236	39649_at
MYH11 (myosin, heavy polypeptide 11, smooth muscle)	AF013570	Hs.78344	NM_002474	16p13.13-p13.12	Cluster Incl. AF013570:Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cd5 /cds=(0,1767) /gb=AF013570 /gl=2352944 /ug=Hs.78344 /len=2580	37407_s_at

PBX3 (pre-B-cell leukemia transcription factor 3)	X59841	Hs.294101	NM_006195	9q33-q34	Cluster Incl. X59841:Human PBX3 mRNA /cds=UNKNOWN /gb=X59841 /gi=35314 /ug=Hs.171680 /len=2581	32696_at
CTSW (cathepsin W (lymphopain))	AF013611	Hs.87450	NM_001335	11q13.1	Cluster Incl. AF013611:Homö sapiens lymphopain mRNA, complete cds /cds=(0,1130) /gb=AF013611 /gi=2582044 /ug=Hs.87450 /len=1131	40718_at
CDW52 (CDW52 antigen (CAMPATH-1 antigen))	N90866	Hs.276770	NM_001803	1p36	Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE- 301723 /clone_end=3 /gb=N90866 /gi=1444193 /ug=Hs.214742 /len=577	34210_at
KIAA0906(KIAA0906 protein)	AB020713	Hs.56966		3	Cluster Incl. AB020713:Homo sapiens mRNA for KIAA0906 protein, partial cds /cds=(0,2772) /gb=AB020713 /gi=4240300 /ug=Hs.56966 /len=4217	41812_s_at
AOE372(thioredoxin peroxidase (antioxidant enzyme))	U25182	Hs.83383	NM_006406	11	Cluster Incl. U25182:Human antioxidant enzyme AOE37-2 mRNA, complete cds /cds=(43,858) /gb=U25182 /gi=799380	38435_at

						/ug=Hs.83383 /len=921	
KIAA0246(KIAA0246 protein), Similar to Mouse notch 3	D87433	Hs.301989	NM_015136	3		Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777	38487_at
HOXB2 (homeo box B2)	X16665	Hs.2733	NM_002145	17q21-q22		Cluster Incl. X16665:Human HOX2H mRNA from the Hox2 locus /cds=(78,1148) /gb=X16665 /gi=32381 /ug=Hs.2733 /len=1520	39610_at
PLXNB2 (plexin B2)	AB002313	Hs.3989		22q13.33		Cluster Incl. AB002313:Human mRNA for KIAA0315 gene, partial cds /cds=(0,5526) /gb=AB002313 /gi=2280475 /ug=Hs.3989 /len=6252	34780_at
SERPINB6 (serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6)	S69272	Hs.41072	NM_004568	6p25		Cluster Incl. S69272:cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt] /cds=(188,1318) /gb=S69272 /gi=546087 /ug=Hs.41072	34789_at

						/len=1465	
EIF4EL3 (eukaryotic translation initiation factor 4E-like 3)	AF038957	Hs.19122	NM_004846	2q37.1	Cluster Incl. AF038957:Homo sapiens translation initiation factor 4e mRNA, complete cds /cds=(58,768) /gb=AF038957 /gi=3329383 /ug=Hs.19122 /len=961	32229_at	
PLCB2 (phospholipase C, beta 2)	M95678	Hs.994	NM_004573	15q15	M95678 /FEATURE= Homo /DEFINITION=HUMPLCB2A sapiens phospholipase C-beta-2 mRNA, complete cds	210_at	
SELL (selectin L (lymphocyte adhesion molecule 1))	M25280	Hs.82848	NM_000655	1q23-q25	M25280 /FEATURE= Human lymph node homing receptor mRNA, complete cds	245_at	
NDUFC1 (NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (8kD, KFY1))	AA760866	Hs.84549	NM_002494	4q28.2-q31.1	Cluster Incl. AA760866:nz14h07.s1 Homo sapiens cDNA /clone=IMAGE-1287805 /gb=AA760866 /gi=2809796 /ug=Hs.84549	38485_at	

					/len=553	
PIG6(proline oxidase homolog)	AF010310	Hs.274550			Cluster Incl. AF010310: Homo sapiens p53 induced protein mRNA, partial cds /cds=(0,761) /gb=AF010310 /gi=2415296 /ug=Hs.211605 /len=888	34110_g_at
HLA-DRA (major histocompatibility complex, class II, DR alpha)	J00194	Hs.76807	NM_019111	6p21.3	Cluster Incl. J00194: human hla-dr antigen alpha-chain mRNA & ivs fragments /cds=(26,790) /gb=J00194 /gi=188231 /ug=Hs.76807 /len=1199	37039_at
					Cluster Incl. M13560: Human le-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518 /ug=Hs.84298 /len=2080	35016_at
POU4F1 (POU domain, class 4, transcription factor 1)	L20433	Hs.211588	NM_006237	13q21.1-q22	Cluster Incl. L20433: Human octamer binding transcription factor 1 (OTF-1) mRNA, complete cds /cds=(234,1496) /gb=L20433 /gi=418015 /ug=Hs.211588	35939_s_at

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						/len=3824		
XBP1 (X-box binding protein 1)	Z93930	Hs.149923	NM_005080	22q12.1	Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs; GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802	39756_g_at		
NDUF85 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDHI))	AF047181	Hs.19236	NM_002492	3q25.1-q25.33	Cluster Incl. AF047181:Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-SGDH mRNA, complete cds /cds=(6,575) /gb=AF047181 /gi=2909853 /ug=Hs.19236 /len=1034	32232_at		
					Cluster Incl. AF052169:Homo sapiens clone 24775 mRNA sequence /cds=UNKNOWN /gb=AF052169	38972_at		

						/gi=3360480 /ug=Hs.109438 /len=1385	
TIP30(Tal-interacting protein (30kD)	AF039103	Hs.90753	NM_006410	11		Cluster Incl. AF039103:Homo sapiens Tal-interacting protein TIP30 mRNA, complete cds /cds=(12,740) /gb=AF039103 /gi=3043926 /ug=Hs.90753 /len=1297	38824_at
HOXA9 (homeo box A9)	U41813	Hs.127428	NM_002142	7p15-p14		Cluster Incl. U41813:Human class I homeoprotein (HOXA9) mRNA, partial cds /cds=(0,389) /gb=U41813 /gi=1184168 /ug=Hs.127428 /len=1411	37809_at
VCL (vinculin)	M33308	Hs.75350	NM_003373	10q22.1-q23		Cluster Incl. M33308:Human vinculin mRNA, complete cds /cds=(50,3250) /gb=M33308 /gi=340236 /ug=Hs.75350 /len=5102	36601_at
DUSP6 (dual specificity phosphatase 6)	AB013382	Hs.180383	NM_001946	12q22-q23		Cluster Incl. AB013382:Homo sapiens mRNA for DUSP6, complete cds /cds=(351,1496) /gb=AB013382 /gi=3869139 /ug=Hs.180383 /len=2390	41193_at

PIG8(eloposide induced 2.4 mRNA)	AF010313	Hs.286027	NM_004879	11	Cluster Incl. AF010313:Homo sapiens PIG8 (PIG8) mRNA, complete cds /cds=(72,1028) /gb=AF010313 /gi=2415301 /ug=Hs.8141 /len=2165	38097_at
SNRPN (small nuclear ribonucleoprotein polypeptide N)	U41303	Hs.48375	NM_003097	15q12	Cluster Incl. U41303:Human small nuclear ribonucleoprotein particle N (SNRPN) mRNA, complete cds - /cds=(465,1187) /gb=U41303 /gi=1145774 /ug=Hs.48375 /len=1326	34842_at
TBC1D1 (TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1)	AB029031	Hs.278586		4	Cluster Incl. AB029031:Homo sapiens mRNA for KIAA1108 protein, partial cds /cds=(0,2291) /gb=AB029031 /gi=5689552 /ug=Hs.69472 /len=2576	32506_at
STAT12(cytokine inducible SH2-containing protein 2)	AF037989	Hs.110776	NM_003877	12	Cluster Incl. AF037989:Homo sapiens STAT-induced STAT inhibitor-2 mRNA, complete cds /cds=(317,913) /gb=AF037989 /gi=3265032 /ug=Hs.110776 /len=1937	38994_at

GNA15 (guanine nucleotide binding protein (G protein), alpha 15 (Gq class))	M63904	Hs.73797	NM_002068	19p13.3	Cluster Incl. M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891 /ug=Hs.73797 /len=2060	40365_at
BZRP (benzodiazepine receptor (peripheral))	M36035	Hs.202	NM_000714	22q13.31	Cluster Incl. M36035:Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds /cds=(61,570) /gb=M36035 /gi=184333 /ug=Hs.202 /len=811	32806_at
NPR3 (natriuretic peptide receptor C(guanylate cyclase C (atrionatriuretic peptide receptor C))	M59305	Hs.123655	NM_000908	5p14-p13	Cluster Incl. M59305:Human atrial natriuretic peptide clearance receptor (ANP C-receptor) mRNA, complete cds /cds=(362,1987) /gb=M59305 /gi=178651 /ug=Hs.123655 /len=2081	34519_at
AGRN (agrin)	AF016903	Hs.273330		1p36.3-p32	Cluster Incl. AF016903:Homo sapiens agrin precursor mRNA, partial cds /cds=(0,6080) /gb=AF016903 /gi=2988421 /ug=Hs.234137 /len=7032	33454_at

EPB41L2 (erythrocyte membrane protein band 4.1-like 2)	AF027299	Hs.7857	NM_001431	6q23	Cluster Incl. AF027299:Homo sapiens protein 4.1-G mRNA, complete cds /cds=(44,3061) /gb=AF027299 /gi=2739095 /ug=Hs.7857 /len=4316	32585_at
S100A8 (S100 calcium-binding protein A8 (calgranulin A))	A1126134	Hs.100000	NM_002964	1q21	Cluster Incl. A1126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 - /gb=A1126134 /gi=3594648 /ug=Hs.100000 /len=446	41096_at
POU4F1 (POU domain, class 4, transcription factor 1)	X64624	Hs.211588	NM_006237	13q21.1-q22	Cluster Incl. X64624:H.sapiens mRNA for RDC-1 POU domain containing protein /cds=(277,1272) /gb=X64624 /gi=35914 /ug=Hs.211588 /len=3492	35940_at
LAK-4P(expressed in activated T/LAK lymphocytes)	AB002405	Hs.16165	NM_007267	17	Cluster Incl. AB002405:Homo sapiens mRNA for LAK-4p, complete cds /cds=(108,1149) /gb=AB002405 /gi=2760120 /ug=Hs.16165 /len=1376	32116_at

ITGB2 (Integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophageantigen 1 (mac-1) beta subunit))	M15395	Hs.83968	NM_000211	21q22.3	Cluster Incl. M15395:Human leukocyte adhesion protein (LFA-1Mac-1/p150,95 family) beta subunit mRNA /cds=(72,2381) /gb=M15395 /gi=186933 /ug=Hs.83968 /len=2776	37918_at
NAGA (N-acetylgalactosaminidase, alpha-)	Z99716	Hs.75372	NM_000262	22q11	Cluster Incl. Z99716:bK250D10.5 (alpha-N-acetylgalactosaminidase) /cds=(472,1707) /gb=Z99716 /gi=4458457 /ug=Hs.75372 /len=3606	36607_at
KLF4 (Kruppel-like factor 4 (gut))	U70663	Hs.7934	NM_004235	9q31	Cluster Incl. U70663:Human zinc finger transcription factor hEZF (EZF) mRNA, complete cds /cds=(503,1915) /gb=U70663 /gi=1857160 /ug=Hs.236377 /len=1953	36214_at
SIPA1 (signal-induced proliferation-associated gene 1)	AB005666	Hs.7019	NM_006747	11q13.3	Cluster Incl. AB005666:Homo sapiens mRNA for GTPase-activating protein, complete cds /cds=(296,3424) /gb=AB005666 /gi=2389008 /ug=Hs.7019	36843_at

						/len=3885		
SPC18(signal peptidase complex (18kD))	AI357653	Hs.9534	NM_014300	15		Cluster Incl. AI357653:qy15c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2012084 /clone_end=3 /gb=AI357653 /gi=4109274 /ug=Hs.9534 /len=833	39139_at	
KIAA0223(minor histocompatibility antigen HA-1)	D86976	Hs.196914		19		Cluster Incl. D86976:Human mRNA for KIAA0223 gene, partial cds /cds=(0,3498) /gb=D86976 /gi=1504025 /ug=Hs.196914 /len=4121	33748_at	
CALR (calreticulin)	M84739	Hs.16488	NM_004343	19p13.3-p13.2		Cluster Incl. M84739:Human autoantigen calreticulin mRNA, complete cds /cds=(108,1361) /gb=M84739 /gi=179881 /ug=Hs.75525 /len=1937	32543_at	
MGC2747(hypothetical protein MGC2747	AL046940	Hs.250723	NM_024104	19		Cluster Incl. AL046940:DKFZp58610517_r1 Homo sapiens cDNA, 5 end /clone=DKFZp58610517 /clone_end=5	41273_at	

SDR1(retinal dehydrogenase/reductase 1)	short-chain	AF061741	Hs.17144	NM_004753	1	Cluster Incl. AF061741: Homo sapiens retinal dehydrogenase/reductase mRNA, complete cds /gb=AF061741 /gi=3450827 /ug=Hs.17144 /len=1401	40782_at
CBFA2T1 (core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related)		D43638	Hs.31551	NM_004349	8q22	Cluster Incl. D43638: Human mRNA for MTC8a protein, complete cds /cds=(411,2144) /gb=D43638 /gi=940399 /ug=Hs.31551 /len=3460	35638_at
CPA3 (carboxypeptidase A3 (mast cell))		M73720	Hs.646	NM_001670	3q21-q25	Cluster Incl. M73720: Human mast cell carboxypeptidase A (MC-CPA) gene /cds=(11,1264) /gb=M73720 /gi=187441 /ug=Hs.646 /len=1633	36749_at

XBP1 (X-box binding protein 1)	Z93930	Hs.149923	NM_005080	22q12.1	Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802	39755_at
DEK (DEK oncogene (DNA binding))	X64229	Hs.110713	NM_003472	6p23	Cluster Incl. X64229:H.sapiens dek mRNA /cds=(33,1160) /gb=X64229 /gi=30502 /ug=Hs.110713 /len=2699	38992_at
PTGER2 (prostaglandin E receptor 2 (subtype EP2), 53kD)	U19487	Hs.2090	NM_000956	14q22	U19487 /FEATURE= Human prostaglandin E2 receptor mRNA, complete cds	828_at
HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814	38095_i_at

						/len=1501	
HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501	38096_f_at	
MPO (myeloperoxidase)	M19507	Hs.1817	NM_000250	17q23.1	Cluster Incl. M19507:Human myeloperoxidase mRNA, complete cds /cds=UNKNOWN /gb=M19507 /gi=188657 /ug=Hs.1817 /len=3215	33284_at	
HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1)	X00457	Hs.914		6p21.3	Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048	38833_at	
AHR (aryl hydrocarbon receptor)	L19872	Hs.170087	NM_001621	7p15	Cluster Incl. L19872:Human AHR-receptor mRNA, complete cds /cds=(375,2921) /gb=L19872 /gi=416141 /ug=Hs.170087	40516_at	

						/len=5228	
DKFZP564K0822(hypothetical protein DKFZp564K0822)	W25986	Hs.4750	NM_030796	7		Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	34830_at
HOXA7 (homeo box A7)	AC004080	Hs.70954	NM_006896	7p15-p14		Cluster Incl. AC004080:Homo sapiens PAC clone DJ0170019 from 7p15-p21 /cds=(0,1247) /gb=AC004080 /gi=2822164 /ug=Hs.110637 /len=1248	41448_at
						Cluster Incl. AL096717:Homo sapiens mRNA; cDNA DKFZp564P0662 (from clone DKFZp564P0662) /cds=UNKNOWN /gb=AL096717 /gi=5419852 /ug=Hs.24178 /len=2228	41328_s_at
S100A9 (S100 calcium-binding protein A9 (calgranulin B))	W72424	Hs.112405	NM_002965	1q21		Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE- 345592 /clone_end=3 /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604	41471_at

CHD3 (chromodomain helicase DNA binding protein 3)	U91543	Hs.25601	NM_001272	17p13.1	Cluster Incl. U91543:Homo sapiens zinc-finger helicase (hZFH) mRNA, complete cds /cds=(150,6152) /gb=U91543 /gi=3298561 /ug=Hs.237761 /len=6771	34707_at
PPIB (peptidylprolyl isomerase B (cyclophilin B))	M63573	Hs.699	NM_000942	15q21-q22	Cluster Incl. M63573:Human secreted cyclophilin-like protein (SCYLP) mRNA, complete cds /cds=(21,671) /gb=M63573 /gi=337998 /ug=Hs.699 /len=893	35823_at
HLA-DMB (major histocompatibility complex, class II, DM beta)	U15085	Hs.1162	NM_002118	6p21.3	Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162 /len=1362	41609_at
TNFAIP3 (tumor necrosis factor, alpha-induced protein 3)	M59465	Hs.211600	NM_006290	6q23.1-q25.3	M59465 /FEATURE= /DEFINITION=HUMA20 Human tumor necrosis factor alpha inducible protein A20 mRNA, complete cds	595_at
LGALS9 (lectin, galactoside-binding, soluble, 9 (galectin 9))	AB006782	Hs.81337	NM_002308	17	AB006782 /FEATURE= /DEFINITION=AB006782 Homo sapiens	766_at

(galectin 9))						mRNA for galectin-9 isoform, complete cds	
RAD23A (RAD23 (S. cerevisiae) homolog A)	D21235	Hs.180455	NM_005053	19p13.2		Cluster Incl. D21235:Human mRNA for HHR23A protein, complete cds /cds=(36,1127) /gb=D21235 /gi=488145 /ug=Hs.180455 /len=1719	41197_at
SLC7A7 (solute carrier family 7 (cationic amino acid transporter, y+ system), member 7)	AJ130718	Hs.194693	NM_003982	14q11.2		Cluster Incl. AJ130718:Human sapiens mRNA for glycoprotein-associated amino acid transporter y+LAT1 /cds=(293,1828) /gb=AJ130718 /gi=3970724 /ug=Hs.194693 /len=2214	33731_at
BMI1 (murine leukemia viral (bmi-1) oncogene homolog)	L13689	Hs.431	NM_005180	10p13		Cluster Incl. L13689:Human prot-oncogene (BMI-1) mRNA, complete cds /cds=(479,1459) /gb=L13689 /gi=291872 /ug=Hs.431 /len=3203	41562_at
DDOST (dolichyl-diphosphooligosaccharide-protein glycosyltransferase)	D29843	Hs.34789	NM_005216	1p36.1		Cluster Incl. D29843:Human mRNA for KIAA0115 gene, complete cds /cds=(106,1476) /gb=D29843 /gi=473936	38791_at

						/ug=Hs.89674 /len=1668	
CEACAM6 (carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen))	M18728	Hs.73848	NM_002483	19q13.2	Cluster Incl. M18728:Human nonspecific crossreacting antigen mRNA, complete cds /cds=UNKNOWN /gb=M18728 /gi=189084 /ug=Hs.73848 /len=2533	36105_at	
TPM4 (tropomyosin 4)	X05276	Hs.250641	NM_003290	19p13.1	Cluster Incl. X05276:Human mRNA for fibroblast tropomyosin TM30 (pl) /cds=(50,796) /gb=X05276 /gi=37201 /ug=Hs.239804 /len=2049	33866_at	
CD34 (CD34 antigen)	M81945	Hs.85289	NM_001773	1q32	Cluster Incl. M81945:Human CD34 gene, promoter and /cds=(258,1415) /gb=M81945 /gi=409018 /ug=Hs.85289 /len=2616	38747_at	
HLA-DRB1 (major histocompatibility complex, class II, DR beta 1)	M32578	Hs.180255	NM_002124	6p21.3	Cluster Incl. M32578:Human MHC class II HLA-DR beta-1 mRNA (DR2.3), 5'end /cds=(61,861) /gb=M32578 /gi=188305 /ug=Hs.181366 /len=1216	41723_s_at	

SIAT4C (sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase))	X74570	Hs.75268	NM_006278	11q23-q24	Cluster Incl. X74570:H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase /cds=(162,1151) /gb=X74570 /gi=414890 /ug=Hs.75268 /len=1741	36916_at
RGS10 (regulator of G-protein signalling 10)	AF045229	Hs.82280	NM_002925	10q25	Cluster Incl. AF045229:Homo sapiens regulator of G protein signaling 10 mRNA, complete cds /cds=(132,635) /gb=AF045229 /gi=2906029 /ug=Hs.82280 /len=753	33121_g_at
EBI2 (Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor))	L08177	Hs.784	NM_004951	13	L08177 /FEATURE= /DEFINITION=HUMGPCRB Human EBV induced G-protein coupled receptor (EBI2) mRNA, complete cds	931_at
NUCB1 (nucleobindin 1)	M96824	Hs.172609	NM_006184	19q13.2-q13.4	Cluster Incl. M96824:Human nucleobindin precursor mRNA, complete cds /cds=(39,1421) /gb=M96824 /gi=189307 /ug=Hs.172609 /len=1650	40817_at

PGRMC1 (progesterone receptor membrane component 1)	Y12711	Hs.90061	NM_006667	xq22-q24	Cluster Incl. Y12711:H.sapiens mRNA for putative progesterone binding protein /cds=(51,638) /gb=Y12711 /gi=2062021 /ug=Hs.90061 /len=1924	38802_at
CEACAM8 (carcinoembryonic antigen-related cell adhesion molecule 8)	M33326	Hs.41	NM_001816	19q13.2	Cluster Incl. M33326:Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds /cds=(86,1135) /gb=M33326 /gi=189101 /ug=Hs.41 /len=2287	33530_at
HLA-DMA (major histocompatibility complex, class II, DM alpha)	X62744	Hs.77522	NM_006120	6p21.3	Cluster Incl. X62744:Human RING6 mRNA for HLA class II alpha chain-like product /cds=(45,830) /gb=X62744 /gi=36062 /ug=Hs.77522 /len=1079	37344_at
DKFZP586N1922(DKFZP586N1922 protein	N99340	Hs.7357		19	Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE-20074 /gb=N99340 /gi=1270755 /ug=Hs.7357 /len=1110	36095_at

SLC9A3R1 (solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1)	AF015926	Hs.184276	NM_004252	17	Cluster Incl. AF015926:Homo sapiens ezrin-radixin-moesin phosphoprotein-50 mRNA, complete cds /cds=(212,1288) /gb=AF015926 /gi=3220018 /ug=Hs.184276 /len=1984	32174_at
MEL (mel transforming oncogene (derived from cell line NK14)- RAB8 homolog)	AI819948	Hs.5947	NM_005370	19p13.1	Cluster Incl. AI819948:wj88e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2409932 /clone_end=3 /gb=AI819948 /gi=5439027 /ug=Hs.5947 /len=569	35340_at
LYPLA1 (lysophospholipase I)	AF081281	Hs.12540	NM_006330	6pter-p25.1	Cluster Incl. AF081281:Homo sapiens lysophospholipase (LPL1) mRNA, complete cds /cds=(35,727) /gb=AF081281 /gi=3415122 /ug=Hs.12540 /len=2417	39396_at
PSCDBP (pleckstrin homology, Sec7 and coiled/coil domains, binding protein)	AF068836	Hs.270	NM_004288	2q11.2	Cluster Incl. AF068836:Homo sapiens cytohesin binding protein HE mRNA, complete cds /cds=(33,1112) /gb=AF068836 /gi=3192908 /ug=Hs.270	39804_at

						/len=1771	
						Cluster Incl. M22806:Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene /cds=(66,1592) /gb=M22806 /gj=487831 /ug=Hs.75655 /len=2438	36666_at
CXX1 (CAAX box 1)	Y13374	Hs.250708	NM_003928	xq26		Cluster Incl. Y13374:Homo sapiens mRNA for putatively prenylated protein /cds=(343,972) /gb=Y13374 /gj=2370152 /ug=Hs.239533 /len=1186	33856_at
SERPING1 (serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary))	X54486	Hs.151242	NM_000062	11q12-q13.1		Cluster Incl. X54486:Human gene for C1-inhibitor /cds=(60,1562) /gb=X54486 /gj=29534 /ug=Hs.151242 /len=1827	39775_at
KIAA0088(KIAA0088 protein)	D42041	Hs.76847	NM_014610	11		Cluster Incl. D42041:Human mRNA for KIAA0088 gene, partial cds /cds=(0,2832) /gb=D42041 /gj=577294 /ug=Hs.76847	37040_at

						/len=3820				
MTCP1 (mature T-cell proliferation 1)	Z24459	Hs.3548	NM_014221	xq28		Cluster Incl. Z24459:H.sepiens MTCP1 gene, exons 2A to 7 (and joined mRNA) /cds=(1419,1625) /gb=Z24459 /gi=2252491 /ug=Hs.3548 /len=1847	35688_g_at			
NFKBIA (nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha)	M69043	Hs.81328	NM_020529	14q13		M69043 /FEATURE= /DEFINITION=HUMMAD3A Homo sapiens MAD-3 mRNA encoding IKB-like activity, complete cds	1461_at			
MST1 (macrophage stimulating 1 (hepatocyte growth factor-like))	U37055	Hs.278657	NM_020998	3p21		U37055 /FEATURE=mRNA Human /DEFINITION=HSU37055 Human hepatocyte growth factor-like protein gene, complete cds	1047_s_at			
ABR (active BCR-related gene)	U01147	Hs.118021	NM_001092	17p13.3		Cluster Incl. U01147:Human guanine nucleotide regulatory protein (ABR) mRNA, complete cds /cds=(110,2689) /gb=U01147 /gi=393094 /ug=Hs.118021	39058_at			

						/len=5242	
TRA1 (tumor rejection antigen (gp96) 1)	X15187	Hs.82689	NM_003299	12q24.2-q24.3	X15187 /DEFINITION=HSTRA1 mRNA for human homologue of murine tumor rejection antigen gp96	/FEATURE=cds Human tra1	442_at
CEBPD (CCAAT/enhancer binding protein (C/EBP), delta)	M83667	Hs.76722	NM_005195	8p11.2-p11.1	M83667 /DEFINITION=HUMNFIL6BA IL6-beta protein mRNA, complete cds	/FEATURE=mRNA Human NF-	1052_s_at

Table 14:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
CAMP (cathelicidin antimicrobial peptide)	Z38026	Hs.51120	NM_004345	3p21.3	Cluster Incl. Z38026; H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	36710_at
MYH11 (myosin, heavy polypeptide 11, smooth muscle)	AF001548	Hs.78344	NM_002474	16p13.13-p13.12	AF001548 /FEATURE=mRNA /DEFINITION=HUA001548 Human Chromosome 16 BAC clone CIT987SK-A- 815A9, complete sequence	767_at
MYH11 (myosin, heavy polypeptide 11, smooth muscle)	AF013570	Hs.78344	NM_002474	16p13.13-p13.12	Cluster Incl. AF013570; Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944	37407_s_at

						/ug=Hs.78344 /len=2580	
SYNE-1B(synaptic nuclear envelope 1)	AB018339					Cluster Incl. AB018339:Homo sapiens mRNA for KIAA0796 protein, partial cds /cds=(0,3243) /gb=AB018339 /gi=3882312 /ug=Hs.8182 /len=3900	38113_at
	K03000	Hs.76392	NM_000689	9q21		Cluster Incl. K03000:Human aldehyde dehydrogenase 1 mRNA /cds=(0,1022) /gb=K03000 /gi=178399 /ug=Hs.76392 /len=1560	37015_at
ARHGAP4 (Rho GTPase activating protein 4)	X78817	Hs.3109	NM_001666	xq28		Cluster Incl. X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817 /gi=840785 /ug=Hs.3109 /len=3236	39649_at
LIG1 (ligase I, DNA, ATP-dependent)	AL039458	Hs.4193		3p14		Cluster Incl. AL039458:DKFZp434N0910_s1 sapiens cDNA, 3 end /clone=DKFZp434N0910 /clone_end=3 /gb=AL039458 /gi=5408506 /ug=Hs.4193	34800_at

						/len=849	
CTSW (cathepsin W (lymphopain))	AF013611	Hs.87450	NM_001335	11q13.1	Cluster Incl. AF013611:Homo sapiens lymphopain mRNA, complete cds /cds=(0,1130) /gb=AF013611 /gi=2582044 /ug=Hs.87450 /len=1131	40718_at	
LON2 (lipocalin 2 (oncogene 24p3))	A1762213	Hs.204238	NM_005564	9q34	Cluster Incl. A1762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=A1762213 /gi=5177880 /ug=Hs.204238 /len=677	32821_at	
CCR2 (chemokine (C-C motif) receptor 2)	U95626			3p21	Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607	37149_s_at	
PBX3 (pre-B-cell leukemia transcription factor 3)	X59841	Hs.294101	NM_006195	9q33-q34	Cluster Incl. X59841:Human PBX3 mRNA /cds=UNKNOWN /gb=X59841 /gi=35314	32696_at	

						/ug=Hs.171680 /len=2581	
CBX7 (chromobox homolog 7)	AL031846	Hs.395	NM_000647	22q13.1		Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gj=4164368 /ug=Hs.7442 /len=3964	36894_at
SGP28(specific granule protein (28 kDa); cysteine-rich secretory protein-3)	X94323	Hs.54431	NM_008061			Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gj=1213612 /ug=Hs.54431 /len=2124	36464_at
PLCE2 (phospholipase C, epsilon 2)	AB029015	Hs.54886		3p25.3-p25.1		Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds /cds=(0,3464) /gb=AB029015 /gj=5689520 /ug=Hs.54886 /len=4147	41796_at
KIAA0246(KIAA0246 protein)	D87433	Hs.301989	NM_015136			Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gj=1665760 /ug=Hs.84753 /len=6777	38487_at

PPBP (pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective	M54995	Hs.2164	NM_002704	4q12-q13	Cluster Incl. M54995:Human connective tissue activation peptide III mRNA, complete cds /cds=(66,452) /gb=M54995 /gi=181175 /ug=Hs.2164 /len=673	39209_r_at
KIAA0906(KIAA0906 p	AB020713	Hs.56866			Cluster Incl. AB020713:Homo sapiens mRNA for KIAA0906 protein, partial cds /cds=(0,2772) /gb=AB020713 /gi=4240300 /ug=Hs.56866 /len=4217	41812_s_at
KCNH2 (potassium voltage-gated channel, subfamily H (eag-related), member 2)	AF052728	Hs.188021	NM_000238	7q35-q36	Cluster Incl. AF052728:Homo sapiens HERG-USO (HERG) mRNA, alternatively spliced, partial cds /cds=(0,284) /gb=AF052728 /gi=3549258 /ug=Hs.165664 /len=767	38225_at
CDW52 (CDW52 antigen (CAMPATH-1 antigen))	N90866	Hs.276770	NM_001803	1p36	Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-301723 /clone_end=3 /gb=N90866 /gi=1444193 /ug=Hs.214742 /len=577	34210_at

PLSCR1 (phospholipid scramblase 1)	AB0006746	Hs.198282	NM_021105	3q23	Cluster Incl. AB0006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=(256,1212) /gb=AB0006746 /gi=3510296 /ug=Hs.198282 /len=2077	32775_r_at
PPBP (pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective	M54995	Hs.2164	NM_002704	4q12-q13	Cluster Incl. M54995:Human connective tissue activation peptide III mRNA, complete cds /cds=(66,452) /gb=M54995 /gi=181175 /ug=Hs.2164 /len=673	39208_l_at
PLXNB2 (plexin B2)	AB002313	Hs.3989		22q13.33	Cluster Incl. AB002313:Human mRNA for KIAA0315 gene, partial cds /cds=(0,5526) /gb=AB002313 /gi=2280475 /ug=Hs.3989 /len=6252	34780_at
TRB@ (T cell receptor beta locus)	M12886	Hs.303157		Hs.303157	M12886 /FEATURE= /DEFINITION=HUMTCBY Human T-cell receptor active beta-chain mRNA, complete cds	1105_s_at
NS1-BP(NS1-binding protein)	AB020657	Hs.197298	NM_006469		Cluster Incl. AB020657:Homo sapiens mRNA for KIAA0850 protein, complete cds	33752_at

						/cds=(630,2558) /gb=AB020657 /gi=4240188 /ug=Hs.197298 /len=3682	
XBP1 (X-box binding protein 1)	Z93930	Hs.149923	NM_005080	22q12.1		Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802	39756_q_at
SYNE-2(synaptic nuclear expressed gene 2)	AL080133	Hs.57749	NM_015180			Cluster Incl. AL080133:Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173) /cds=(122,3400) /gb=AL080133 /gi=5262573 /ug=Hs.57749 /len=4307	41815_at
HLA-F (major histocompatibility complex, class I, F)	AL022723	Hs.110309	NM_018950	6p21.3		Cluster Incl. AL022723:dJ377H14.9 (major histocompatibility complex, class I, F (CDA12)) /cds=(97,1185) /gb=AL022723	37420_i_at

					/gi=5002624 /ug=Hs.110309 /len=1303	
AOE372(thioredoxin peroxidase (antioxidant enzyme))	U25182	Hs.83383	NM_006406		Cluster Incl. U25182:Human antioxidant enzyme AOE37-2 mRNA, complete cds /cds=(43,858) /gb=U25182 /gi=799380 /ug=Hs.83383 /len=921	38435_at
SELL (selectin L (lymphocyte adhesion molecule 1))	M25280	Hs.82848	NM_000655	1q23-q25	M25280 /FEATURE= /DEFINITION=HUMLNHR Human lymph node homing receptor mRNA, complete cds	245_at
PF4 (platelet factor 4)	M25897	Hs.81564	NM_002619	4q12-q21	M25897 /FEATURE=mRNA /DEFINITION=HUMPF4A Human platelet factor 4 (PF4) mRNA, complete cds	1115_at
SERPINB6 (serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6)	S69272	Hs.41072	NM_004568	6p25	Cluster Incl. S69272:cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt] /cds=(188,1318) /gb=S69272 /gi=546087 /ug=Hs.41072	34789_at

						/len=1465	
HOXB2 (homeo box B2)	X16665	Hs.2733	NM_002145	17q21-q22	Cluster Incl. X16665:Human HOX2H mRNA from the Hox2 locus /cds=(78,1148) /gb=X16665 /gi=32381 /ug=Hs.2733 /len=1520	39610_at	
S100A8 (S100 calcium-binding protein A8 (calgranulin A))	A1126134	Hs.100000	NM_002964	1q21	Cluster Incl. A1126134:q477c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 /gb=A1126134 /gi=3594648 /ug=Hs.100000 /len=446	41096_at	
CD59 (CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32	M84349	Hs.119863	NM_000611	11p13	Cluster Incl. M84349:Human transmembrane protein (CD59) gene /cds=(18,404) /gb=M84349 /gi=180150 /ug=Hs.119863 /len=1840	39351_at	
GNA15 (guanine nucleotide binding protein (G protein), alpha 15 (Gq class))	M63904	Hs.73797	NM_002068	19p13.3	Cluster Incl. M63904:Human G-alpha.16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891	40365_at	

						/ug=Hs.73797 /len=2060			
PIG6(proline oxidase homolog)	AF010310	Hs.274550				Cluster Incl. AF010310:Homo sapiens p53 induced protein mRNA, partial cds /cds=(0,761) /gb=AF010310 /gi=2415296 /ug=Hs.211605 /len=888	34110_g_at		
	AF052169					Cluster Incl. AF052169:Homo sapiens clone 24775 mRNA sequence /cds=UNKNOWN /gb=AF052169 /gi=3360480 /ug=Hs.109438 /len=1385	38972_at		
EIF4EL3 (eukaryotic translation initiation factor 4E-like 3)	AF038957	Hs.19122			2q37.1	Cluster Incl. AF038957:Homo sapiens translation initiation factor 4e mRNA, complete cds /cds=(58,768) /gb=AF038957 /gi=3329383 /ug=Hs.19122 /len=961	32229_at		
DDOST (dolichyl-diphosphooligosaccharide-protein glycosyltransferase)	D29643	Hs.34789			1p36.1	Cluster Incl. D29643:Human mRNA for KIAA0115 gene, complete cds /cds=(106,1476) /gb=D29643 /gi=473936	38791_at		

						/ug=Hs.89674 /len=1668		
MMP9 (matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase))	J05070	Hs.151738	NM_004994	20q11.2-q13.1	Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334	31859_at		
CALR (calreticulin	M84739	Hs.16488	NM_004343	19p13.3-p13.2	Cluster Incl. M84739:Human autoantigen calreticulin mRNA, complete cds /cds=(108,1361) /gb=M84739 /gi=179881 /ug=Hs.75525 /len=1937	32543_at		
DKFZP564K0822(hypothetical protein DKFZp564K0822)	W25986	Hs.4750	NM_030796		Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	34830_at		
XBP1 (X-box binding protein 1)	Z93930	Hs.149923	NM_005080	22q12.1	Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815)	39755_at		

						/gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802				
VCL (vinculin)	M33308	Hs.75350	NM_003373	10q22.1-q23	Cluster Incl. M33308:Human vinculin mRNA, complete cds /cds=(50,3250) /gb=M33308 /gi=340236 /ug=Hs.75350 /len=5102	36801_at				
POU4F1 (POU domain, class 4, transcription factor 1)	L20433	Hs.211588	NM_006237	13q21.1-q22	Cluster Incl. L20433:Human octamer binding transcription factor 1 (OTF1) mRNA, complete cds /cds=(234,1496) /gb=L20433 /gi=418015 /ug=Hs.211588 /len=3824	35939_s_at				
MIC2 (antigen identified by monoclonal antibodies 12E7, F21 and O13)	M16279	Hs.177543	NM_002414	xp22.32: yp11.3	Cluster Incl. M16279:Human MIC2 mRNA, complete cds /cds=(177,734) /gb=M16279 /gi=188542 /ug=Hs.177543 /len=1238	41138_at				
DEFA4 (defensin, alpha 4, corticostatin)	A1250799	Hs.2582	NM_001925	8p23	Cluster Incl. A1250799:ql36g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-	34546_at				

					1858620 /clone_end=3 /gb=A1250799 /gi=3847328 /ug=Hs.2582 /len=542	
NDUFC1 (NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (GkD, KFYI))	AA760866	Hs.84549	NM_002494	4q28.2-q31.1	Cluster Incl. AA760866:nz14h07.s1 Homo sapiens cDNA /clone=IMAGE-1287805 /gb=AA760866 /gi=2809796 /ug=Hs.84549 /len=553	38485_at
SPTA1 (spectrin, alpha, erythrocytic 1 (eliptocytosis 2))	M61877	Hs.1985	NM_003126	1q21	Cluster Incl. M61877:Human erythroid alpha-spectrin (SPTA1) mRNA, complete cds /cds=(186,7475) /gb=M61877 /gi=338437 /ug=Hs.1985 /len=8001	38906_at
EPB72 (erythrocyte membrane protein band 7.2 (stomatin))	X85116	Hs.160483	NM_004099	9q34.1	Cluster Incl. X85116:H.sapiens epb72 gene exon 1 /cds=(61,927) /gb=X85116 /gi=1161561 /ug=Hs.160483 /len=3035	40419_at
CD24 (CD24 antigen (small cell lung carcinoma cluster 4 antigen))	L33930	Hs.286124	NM_013230	6q21	L33930 /FEATURE= /DEFINITION=HUMCD24B Homo sapiens CD24 signal transducer mRNA, complete cds and 3 region	266_s_at

HOXA9 (homeo box A9)	U41813	Hs.127428	NM_002142	7p15-p14	Cluster Incl. U41813:Human class I homeoprotein (HOXA9) mRNA, partial cds /cds=(0,389) /gb=U41813 /gi=1184168 /ug=Hs.127428 /len=1411	37809_at
HLA-DRA (major histocompatibility complex, class II, DR alpha)	J00194	Hs.76807	NM_019111	6p21.3	Cluster Incl. J00194:human hla-dr antigen alpha-chain mrna & ivs fragments /cds=(26,790) /gb=J00194 /gi=188231 /ug=Hs.76807 /len=1199	37039_at
OLR1 (oxidised low density lipoprotein (lectin-like) receptor 1)	AF079167	Hs.77729	NM_002543	12p13.2-p12.3	Cluster Incl. AF079167:untitled /cds=(61,882) /gb=AF079167 /gi=4050003 /ug=Hs.77729 /len=2468	37233_at
	M1872				Cluster Incl. M1872:Human nonspecific crossreacting antigen mRNA, complete cds /cds=UNKNOWN /gb=M18728 /gi=189084 /ug=Hs.73848 /len=2533	36105_at
DEK (DEK oncogene (DNA binding))	X64229	Hs.110713	NM_003472	6p23	Cluster Incl. X64229:H.sapiens dek mRNA /cds=(33,1160) /gb=X64229 /gi=30502	38992_at

						/ug=Hs.110713 /len=2699	
AGRN (egrin)	AF016903	Hs.273330			1p36.3-p32	Cluster Incl. AF016903:Homo sapiens agrin precursor mRNA, partial cds /cds=(0,6080) /gb=AF016903 /gi=2988421 /ug=Hs.234137 /len=7032	33454_at
PIR121(p53 inducible protein)	L47738	Hs.256503				Cluster Incl. L47738:Homo sapiens inducible protein mRNA, complete cds /cds=(1004,1714) /gb=L47738 /gi=1009098 /ug=Hs.80313 /len=2881	37579_at
ITGB2 (integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage	M15395	Hs.83968		NIM_000211	21q22.3	Cluster Incl. M15395:Human leukocyte adhesion protein (LFA-1/Mac-1/p150,95 family) beta subunit mRNA /cds=(72,2381) /gb=M15395 /gi=186933 /ug=Hs.83968 /len=2776	37918_at
STAT12(cytokine inducible SH2-containing protein 2)	AF037989	Hs.110776		NIM_003877		Cluster Incl. AF037989:Homo sapiens STAT-induced STAT inhibitor-2 mRNA, complete cds /cds=(317,913) /gb=AF037989 /gi=3265032	38994_at

						/ug=Hs.110776 /len=1937	
TBC1D1 (TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1)	AB029031	Hs.278586			4	Cluster Incl. AB029031:Homo sapiens mRNA for KIAA1108 protein, partial cds /cds=(0,2291) /gb=AB029031 /gi=5689552 /ug=Hs.69472 /len=2576	32508_at
DEFA1 (defensin, alpha 1, myeloid-related sequence)	AL036554	Hs.274463	NM_004084		8p23.2-p23.1	Cluster Incl. AL036554:DKFZp564J2262_r1 Homo sapiens cDNA, 5 end /clone=DKFZp564J2262 /clone_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.1379 /len=517	31793_at
MGC2747(hypothetical protein MGC2747)	AL046940	Hs.250723	NM_024104			Cluster Incl. AL046940:DKFZp586I0517_r1 Homo sapiens cDNA, 5 end /clone=DKFZp586I0517 /clone_end=5 /gb=AL046940 /gi=5434999 /ug=Hs.231657 /len=695	41273_at

LILRB2 (leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains),	AF004231	Hs.22405	NM_005874	19q13.4	Cluster Incl. AF004231:Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds /cds=(208,2001) /gb=AF004231 /gi=2343110 /ug=Hs.22405 /len=2863	39221_at
CPA3 (carboxypeptidase A3 (mast cell))	M73720	Hs.646	NM_001870	3q21-q25	Cluster Incl. M73720:Human mast cell carboxypeptidase A (MC-CPA) gene /cds=(11,1264) /gb=M73720 /gi=187441 /ug=Hs.646 /len=1633	36749_at
	M13560				Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518 /ug=Hs.84288 /len=2080	35016_at
	M3332				Cluster Incl. M3332:Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds /cds=(86,1135) /gb=M33326 /gi=189101 /ug=Hs.41 /len=2287	33530_at

DEFA3 (defensin, alpha 3, neutrophil-specific)	L12691	Hs.294176	NM_005217	8pter-p23.3	Cluster Incl. L12691:Human neutrophil peptide-3 gene, complete cds /cds=(50,334) /gb=L12691 /gi=292364 /ug=Hs.178741 /len=452	31506_s_at
PLXNC1 (plexin C1)	AF030339	Hs.286229	NM_005761	12	Cluster Incl. AF030339:Homo sapiens receptor for viral semaphorin protein (VESPR) mRNA, complete cds /cds=(249,4955) /gb=AF030339 /gi=3176761 /ug=Hs.184697 /len=5121	32193_at
	U7066				Cluster Incl. U70663:Human zinc finger transcription factor hEZF (EZF) mRNA, complete cds /cds=(503,1915) /gb=U70663 /gi=1857160 /ug=Hs.236377 /len=1953	36214_at
	AF035315				Cluster Incl. AF035315:Homo sapiens clone 23664 and 23905 mRNA sequence /cds=UNKNOWN /gb=AF035315 /gi=2661077 /ug=Hs.180737 /len=1331	33267_at

CTSE (cathepsin E)	J05036	Hs.1355	NM_001910	1q31	J05036 /DEFINITION=HUMCTSE cathepsin E mRNA, complete cds	/FEATURE=mRNA Human	271_s_at
NDUFB5 (NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGDHI))	AF047181	Hs.19236	NM_002492	3q25.1-q25.33	Cluster Incl. AF047181: Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-SGDH mRNA, complete cds /cds=(6,575) /gb=AF047181 /gi=2909853 /ug=Hs.19236 /len=1034		32232_at
S100A9 (S100 calcium-binding protein A9 (calgranulin B))	W72424	Hs.112405	NM_002965	1q21	Cluster Incl. W72424: zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE- 345592 /clone_end=3 /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604		41471_at
SNRPN (small nuclear ribonucleoprotein polypeptide N)	U41303	Hs.48375	NM_003097	15q12	Cluster Incl. U41303: Human small nuclear ribonucleoprotein particle N (SNRPN) mRNA, complete cds /cds=(465,1187) /gb=U41303 /gi=1145774 /ug=Hs.48375 /len=1326		34842_at

SLU7(step II splicing factor SLU7)	AI660656	Hs.76325	NM_006425		Cluster Incl. AI660656:wf23c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2351436 /clone_end=3 /gb=AI660656 /gi=4764239 /ug=Hs.76325 /len=522	37006_at
ADD2 (adducin 2 (beta))	U43959	Hs.247423	NM_001617	2p14-p13	Cluster Incl. U43959:Human beta 4 adducin mRNA, alternatively spliced partial cds /cds=(0,938) /gb=U43959 /gi=1172145 /ug=Hs.4852 /len=1284	36052_at
DF (D component of complement (adipsin))	M84526	Hs.155597	NM_001928	19	Cluster Incl. M84526:Human adipsin/complement factor D mRNA, complete cds /cds=(54,740) /gb=M84526 /gi=178625 /ug=Hs.155597 /len=1071	40282_s_at
PLCB2 (phospholipase C, beta 2)	M95678	Hs.994	NM_004573	15q15	M95678 /FEATURE= /DEFINITION=HUMPLCB2A Homo sapiens phospholipase C-beta-2 mRNA, complete cds	210_at
POU4F1 (POU domain, class 4, transcription factor 1)	X64624	Hs.211588	NM_006237	13q21.1-q22	Cluster Incl. X64624:H.sapiens mRNA for RDC-1 POU domain containing protein	35940_at

factor 1)						/cds=(277,1272) /gb=X64624 /gi=35914 /ug=Hs.211588 /len=3492		
PPIB (peptidylprolyl isomerase B (cyclophilin B))	M63573	Hs.699	NM_000942	15q21-q22		Cluster Incl. M63573:Human secreted cyclophilin-like protein (SCYLP) mRNA, complete cds /cds=(21,671) /gb=M63573 /gi=337998 /ug=Hs.699 /len=893	35823_at	
KIAA0088(KIAA0088 protein)	D42041	Hs.76847	NM_014610			Cluster Incl. D42041:Human mRNA for KIAA0088 gene, partial cds /cds=(0,2832) /gb=D42041 /gi=577294 /ug=Hs.76847 /len=3820	37040_at	
LAK-4P(expressed in activated T/LAK lymphocytes)	AB002405	Hs.16165	NM_007267			Cluster Incl. AB002405:Homo sapiens mRNA for LAK-4p, complete cds /cds=(109,1149) /gb=AB002405 /gi=2760120 /ug=Hs.16165 /len=1376	32116_at	
TFDP1 (transcription factor Dp-1)	L23959	Hs.79353	NM_007111	13q34		Cluster Incl. L23959:Homo sapiens E2F- related transcription factor (DP-1) mRNA, complete cds /cds=(37,1269) /gb=L23959	37757_at	

						/gi=414316 /ug=Hs.79353 /len=1440	
CPO (coproporphyrinogen oxidase (coproporphyrin, harderoporphyria))	D16611	Hs.89866	NM_000097	3q12		Cluster Incl. D16611:Human mRNA for coproporphyrinogen oxidase, complete cds /cds=(93,1157) /gb=D16611 /gi=469488 /ug=Hs.89866 /len=2333	37999_at
MMP8 (matrix metalloproteinase 8 (neutrophil collagenase))	J05556	Hs.73862	NM_002424	11q22.3		J05556 /FEATURE=mRNA /DEFINITION=HUMCLGNA Homo sapiens collagenase mRNA, complete cds	681_at
DUSP6 (dual specificity phosphatase 6)	AB013382	Hs.180383	NM_001946	12q22-q23		Cluster Incl. AB013382:Homo sapiens mRNA for DUSP6, complete cds /cds=(351,1496) /gb=AB013382 /gi=3869139 /ug=Hs.180383 /len=2390	41193_at
NPR3 (natriuretic peptide receptor C/guanylate cyclase C (atrialnatriuretic peptide receptor C))	M59305	Hs.123655	NM_000908	5p14-p13		Cluster Incl. M59305:Human atrial natriuretic peptide clearance receptor (ANP C-receptor) mRNA, complete cds /cds=(362,1987) /gb=M59305 /gi=178651 /ug=Hs.123655 /len=2081	34519_at

MPO (myeloperoxidase)	M19507	Hs.1817	NM_000250	17q23.1	Cluster Incl. M19507:Human myeloperoxidase mRNA, complete cds /cds=UNKNOWN /gb=M19507 /gi=188657 /ug=Hs.1817 /len=3215	33284_at
MINPP1 (multiple inositol polyphosphate histidine phosphatase, 1)	AL050356	Hs.95907	NM_004897	10q23	Cluster Incl. AL050356: Homo sapiens mRNA; cDNA DKFZp564L2016 (from clone DKFZp564L2016) /cds=UNKNOWN /gb=AL050356 /gi=4914568 /ug=Hs.95907 /len=2396	38325_at
	S67247				Cluster Incl. S67247: smooth muscle myosin heavy chain isoform SMemb [human, umbilical cord, fetal aorta, mRNA Partial, 971 nt] /cds=(0,681) /gb=S67247 /gi=452986 /ug=Hs.2094 /len=971	32838_at
TPM4 (tropomyosin 4)	X05276	Hs.250641	NM_003290	19p13.1	Cluster Incl. X05276: Human mRNA for fibroblast tropomyosin TM30 (pl) /cds=(50,796) /gb=X05276 /gi=37201 /ug=Hs.239804 /len=2049	33866_at

CBFA2T1 (core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related)	D43638	Hs.31551	NM_004349	8q22	Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /cds=(411,2144) /gb=D43638 /gi=940399 /ug=Hs.31551 /len=3460	35638_at
LEF1 (lymphoid enhancer-binding factor 1)	AL049409	Hs.44865	NM_016269	4q23-q25	Cluster Incl. AL049409:Human sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419	36021_at
AHR (aryl hydrocarbon receptor)	L19872	Hs.170087	NM_001621	7p15	Cluster Incl. L19872:Human AH-receptor mRNA, complete cds /cds=(375,2921) /gb=L19872 /gi=416141 /ug=Hs.170087 /len=5228	40516_at
SERPINC1 (serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1,	X54486	Hs.151242	NM_000062	11q12-q13.1	Cluster Incl. X54486:Human gene for C1-inhibitor /cds=(60,1562) /gb=X54486 /gi=29534 /ug=Hs.151242 /len=1827	39775_at
PIG8(etoposide induced 2.4 mRNA)	AF010313	Hs.286027	NM_004879		Cluster Incl. AF010313:Human sapiens PIG8 (PIG8) mRNA, complete cds	38097_at

						/cds=(72,1028) /gb=AF010313 /gi=2415301 /ug=Hs.8141 /len=2165	
SEPT3 (septin 3)	Z99716	Hs.8073	NM_019106	22q13.2	Cluster Incl. Z99716:bk250D10.5 (alpha-N-acetylglucosaminidase) /cds=(472,1707) /gb=Z99716 /gi=4456457 /ug=Hs.75372 /len=3606	36607_at	
TPM1 (tropomyosin 1 (alpha))	M19267	Hs.77899	NM_000366	15q22.1	Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1140) /gb=M19267 /gi=339943 /ug=Hs.77899 /len=1633	36791_g_at	
AMPD3 (adenosine monophosphate deaminase (isoform E))	U29926	Hs.83918	NM_000480	11p15	Cluster Incl. U29926:Human AMP deaminase (AMPD3) gene, promoter 1a region /cds=(453,2777) /gb=U29926 /gi=1002661 /ug=Hs.83918 /len=4018	38463_s_at	

HELO1(homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	AL034374	Hs.250175	NM_021814		Cluster Incl. AL034374:Human DNA sequence from clone 483K16 on chromosome 6p12.1-21.1. Contains (parts of) two novel genes, 40S Ribosomal protein S16 and 60S Ribosomal protein L31 pseudogenes, ESTs, STSs, GSSs and a putative CpG island /cds=(0,703) /gb=AL	33821_at
PRKWNK1 (protein kinase, lysine deficient 1)	U00946	Hs.184592	NM_018979	12p13.3	Cluster Incl. U00946:Human clone AGA2BRB5 (CAC)n(GTG)n repeat- containing mRNA /cds=UNKNOWN /gb=U00946 /gi=405048 /ug=Hs.184592 /len=1971	32185_at
EPB41L2 (erythrocyte membrane protein band 4.1-like 2)	AF027299	Hs.7857	NM_001431	6q23	Cluster Incl. AF027299:Homo sapiens protein 4.1-G mRNA, complete cds /cds=(44,3061) /gb=AF027299 /gi=2739095 /ug=Hs.7857 /len=4316	32585_at
CD48 (CD48 antigen (B-cell membrane protein))	M37766	Hs.901	NM_001778	1q21.3-q22	Cluster Incl. M37766:Human MEM-102 glycoprotein mRNA, complete cds	38006_at

						/cds=(20,751) /gb=M37766 /gi=187518 /ug=Hs.901 /len=1058			
PRDX2 (peroxiredoxin 2)		L19185	Hs.146354	NM_005809	13q12	Cluster Incl. L19185:Human natural killer cell enhancing factor- (NKEFB) mRNA, complete cds /cds=(124,720) /gb=L19185 /gi=440307 /ug=Hs.146354 /len=980	39729_at		
TIP30(Tat-interacting protein (30kD)		AF039103	Hs.90753	NM_006410		Cluster Incl. AF039103:Homo sapiens Tat- interacting protein TIP30 mRNA, complete cds /cds=(12,740) /gb=AF039103 /gi=3043926 /ug=Hs.90753 /len=1297	38824_at		
ARG1 (arginase, liver)		M14502	Hs.289057	NM_000045	6q23	M14502 /FEATURE=mRNA /DEFINITION=HUMARGL Human liver arginase mRNA, complete cds	1962_at		
TRA1 (tumor rejection antigen (gp96) 1)		X15187	Hs.82689	NM_003299	12q24.2-q24.3	X15187 /FEATURE=cds /DEFINITION=HSTRA1 Human tra1 mRNA for human homologue of murine tumor rejection antigen gp96	442_at		

HOXA7 (homeo box A7)	AC004080	Hs.70954	NM_006896	7p15-p14	Cluster Incl. AC004080:Homo sapiens PAC clone DJ0170019 from 7p15-p21 /cds=(0,1247) /gb=AC004080 /gi=2822164 /lug=Hs.110637 /len=1248	41448_at
CD34 (CD34 antigen)	M81945	Hs.85289	NM_001773	1q32	Cluster Incl. M81945:Human CD34 gene, promoter and /cds=(258,1415) /gb=M81945 /gi=409018 /lug=Hs.85289 /len=2616	38747_at
SNL (singled (Drosophila)-like (sea urchin fascic homolog like))	U03057	Hs.118400	NM_003088	7p22	Cluster Incl. U03057:Human actin bundling protein (HSN) mRNA, complete cds /cds=(111,1592) /gb=U03057 /gi=458027 /lug=Hs.118400 /len=2767	39070_at
BZRP (benzodiazepine receptor (peripheral))	M36035	Hs.202	NM_000714	22q13.31	Cluster Incl. M36035:Human peripheral benzodiazepine receptor (hpbs) mRNA, complete cds /cds=(61,570) /gb=M36035 /gi=184333 /lug=Hs.202 /len=811	32806_at

SIAT4C (sialyltransferase 4C (beta-galactosidase alpha-2,3-sialyltransferase))	X74570	Hs.75268	NM_006278	11q23-q24	Cluster Incl. X74570:H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc sialyltransferase /cds=(162,1151) /gb=X74570 /gi=414890 /ug=Hs.75268 /len=1741	36916_at
TCF7 (transcription factor 7 (T-cell specific, HMG-box))	X59871	Hs.169294	NM_003202	5q31.1	Cluster Incl. X59871:Human TCF-1 mRNA for T cell factor 1 (splice form C) /cds=(79,885) /gb=X59871 /gi=36789 /ug=Hs.169294 /len=2910	32649_at
HLA-DPB1 (major histocompatibility complex, class II, DP beta 1)	M83664	Hs.814	NM_002121	6p21.3	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501	38095_l_at
BMI1 (murine leukemia viral (bmi-1) oncogene homolog)	L13689	Hs.431	NM_005180	10p13	Cluster Incl. L13689:Human prot-oncogene (BMI-1) mRNA, complete cds /cds=(479,1459) /gb=L13689 /gi=291872 /ug=Hs.431 /len=3203	41562_at

RBM9 (RNA binding motif protein 9)	AL009266	Hs.5011	NM_014309	22q13.1	Cluster Incl. AL009266:H. sapiens cDNA similar to C. elegans RNA binding protein U14946, Q10572, complete cds /cds=(170,1273) /gb=AL009266 /gi=2664428 /ug=Hs.155156 /len=1876	40260_g_at
NUCB1 (nucleobindin 1)	M96824	Hs.172609	NM_006184	19q13.2-q13.4	Cluster Incl. M96824:Human nucleobindin precursor mRNA, complete cds /cds=(39,1421) /gb=M96824 /gi=189307 /ug=Hs.172609 /len=1650	40817_at
IGF2R (insulin-like growth factor 2 receptor)	Y00285	Hs.76473	NM_000876	6q26	Y00285 /FEATURE=cds /DEFINITION=HSGFIIR Human mRNA for insulin-like growth factor II receptor /NOTE=replacement of probe set 972_s_at	160027_s_at
FCN1 (ficolin (collagen/fibrinogen domain-containing) 1)	S80990	Hs.252136	NM_002003	9q34	Cluster Incl. S80990:ficolin [human, uterus, mRNA, 1736 nt] /cds=(532,1512) /gb=S80990 /gi=1911529 /ug=Hs.169237 /len=1723	36447_at

HLA-DPA1 (major histocompatibility complex, class II, DP alpha 1)	X00457	Hs.914		6p21.3	Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048	38833_at
	M22806				Cluster Incl. M22806:Human prolyl 4-hydroxylase beta-subunit and disulfide isomerase (P4HB) gene /cds=(66,1592) /gb=M22806 /gi=487831 /ug=Hs.75655 /len=2438	36866_at
					Cluster Incl. AB011085:Homo sapiens mRNA for KIAA0513 protein, complete cds /cds=(631,1866) /gb=AB011085 /gi=3043549 /ug=Hs.85053 /len=7758	38735_at
MGEA5 (meningioma expressed antigen 5 (hyaluronidase))	AB014579	Hs.5734	NM_012215	10q24.1-q24.3	Cluster Incl. AB014579:Homo sapiens mRNA for KIAA0679 protein, partial cds /cds=(0,2303) /gb=AB014579 /gi=3327171 /ug=Hs.5734 /len=4303	35317_at

Table 15:

UCL/HGNC/HUGO Human Gene Nomenclature Database Symbol	GenBank Accession No.	UniGene Cluster	RefSeq	Chromosomal Location	Description Unigene Build #95	Gene Name
TNFRSF7 (tumor necrosis factor receptor superfamily, member 7)	M63928	Hs.180841	NM_001242	12p13	Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204	38578_at
DKFZP564K0822(hypothetical protein DKFZp564K0822)	W25986	Hs.4750	NM_030796	7	Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	34830_at
PFTK1 (PFTAIRE protein kinase 1)	AB020641	Hs.57856	NM_012395	7q21-q22	Cluster Incl. AB020641:Homo sapiens mRNA for KIAA0834 protein, complete cds /cds=(144,1499) /gb=AB020641 /gi=4240156 /ug=Hs.57856 /len=4957	36502_at

CBX7 (chromobox homolog 7)	AL031846			22q13.1	Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964	36894_at
IGHM (immunoglobulin heavy constant mu)	X58529	Hs.302063		14q32.33	Cluster Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN /gb=X58529 /gi=33480 /ug=Hs.179543 /len=2325	41166_at
PLCE2 (phospholipase C, epsilon 2)	AB029015	Hs.54886		3p25.3-p25.1	Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds /cds=(0,3464) /gb=AB029015 /gi=5689520 /ug=Hs.54886 /len=4147	41796_at
IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41165_g_at

IGHM (immunoglobulin heavy constant mu)	X67301	Hs.302063		14q32.33	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	41164_at
					Cluster Incl. X62822:H.sapiens gene encoding beta-galactoside alpha-2,6-sialyltransferase /cds=(310,1530) /gb=X62822 /gi=29433 /ug=Hs.2554 /len=2699	41352_at
HLA-DOB (major histocompatibility complex, class II, DO beta)	X03066	Hs.1802	NM_002120	6p21.3	Cluster Incl. X03066:Human mRNA for HLA-D class II antigen DO beta chain /cds=(56,877) /gb=X03066 /gi=32271 /ug=Hs.1802 /len=1322	38570_at
	W30677				Cluster Incl. W30677:zb75h10.r1 Homo sapiens cDNA, 5' end /clone=IMAGE-309475 /clone_end=5 /gb=W30677 /gi=1311730 /ug=Hs.5019 /len=614	34871_at

IL24 (interleukin 24)	AA214546	Hs.315463	NM_006850	1q32	Cluster Incl. AA214546:zf92c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-683140 /clone_end=3 /gb=AA214546 /gi=1813171 /ug=Hs.66576 /len=516	41847_at
CELSR1 (cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog)	AL031588	Hs.252387	NM_014246	22q13.3	Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438	41660_at
LOC54103(hypothetical protein)	AL079277	Hs.12969		7	Cluster Incl. AL079277:Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 293605 /cds=(0,806) /gb=AL079277 /gi=5102581 /ug=Hs.12969 /len=1414	41710_at
NIFU(nitrogen fixation cluster-like)	U47101	Hs.9908		12	Cluster Incl. U47101:Human NifU-like protein (hNifU) mRNA, partial cds /cds=(0,366) /gb=U47101 /gi=1685101	39165_at

						/ug=Hs.9908 /len=819			
CD79A (CD79A antigen (immunoglobulin-associated alpha))	U05259	Hs.79630	NM_001783	19q13.2		Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=U05259 /gi=452561 /ug=Hs.79630 /len=1107	38017_at		
SETBP1 (SET binding protein 1)	AB022660	Hs.151717	NM_015559	18q21.1		Cluster Incl. AB022660:Homo sapiens mRNA for SET-binding protein (SEB), complete cds /cds=(5,4633) /gb=AB022660 /gi=5478317 /ug=Hs.151717 /len=5744	34990_at		
NCOA3 (nuclear receptor coactivator 3)	AF012108	Hs.225977	NM_006534	20q12		Cluster Incl. AF012108:Homo sapiens Amplified in Breast Cancer (AIB1) mRNA, complete cds /cds=(200,4462) /gb=AF012108 /gi=2331249 /ug=Hs.225977 /len=6818	33381_at		
POU2AF1 (POU domain, class 2, associating factor 1)	Z49194	Hs.2407	NM_006235	11q23.1		Cluster Incl. Z49194:H.sapiens mRNA for oct-binding factor /cds=(523,1293) /gb=Z49194 /gi=974830 /ug=Hs.2407	36239_at		

					/len=3301	
SYNE-2(synaptic nuclei expressed gene 2)	AL080133	Hs.57749	NM_015180	22	Cluster Incl. AL080133:Homo sapiens mRNA; cDNA DKFZp434G173 (from clone DKFZp434G173) /cds=(122,3400) /gb=AL080133 /gi=5262573 /ug=Hs.57749 /len=4307	41815_at
SP140(nuclear body protein Sp140)	U36500	Hs.309943	NM_007237	2	Cluster Incl. U36500:Human lymphoid-specific SP100 homolog (LYSP100-B) mRNA, complete cds /cds=(116,2764) /gb=U36500 /gi=1173653 /ug=Hs.85283 /len=3252	40700_at
CAMP (cathelicidin antimicrobial peptide)	Z38026	Hs.51120	NM_004345	3p21.3	Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	36710_at
TOSO(regulator of Fas-induced apoptosis)	AF057557	Hs.58831	NM_005449	1	Cluster Incl. AF057557:Homo sapiens anti-Fas-induced apoptosis (TOSO) mRNA, complete cds /cds=(19,1191)	32967_at

						/gb=AF057557 /gj=3169292 /ug=Hs.238857 /len=1339	
TC21(oncogene TC21)	A1365215	Hs.206097	NM_012250	11		Cluster Incl. A1365215;qz41a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2029426 /clone_end=3 /gb=A1365215 /gi=4124904 /ug=Hs.206097 /len=918	32827_at
	A1434146					Cluster Incl. A1434146;ti36g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2132604 /clone_end=3 /gb=A1434146 /gi=4294137 /ug=Hs.164284 /len=299	36403_s_at
DGKA (diacylglycerol kinase, alpha (80kD))	X62535	Hs.172690	NM_001345	12q13.3		Cluster Incl. X62535:H.sapiens mRNA for diacylglycerol kinase /cds=(103,2310) /gb=X62535 /gi=30822 /ug=Hs.172690 /len=2564	32716_at
SAC2(cDNA sequence, clone 3-26)	AB023183	Hs.52463	NM_014937	10		Cluster Incl. AB023183:Homo sapiens mRNA for KIAA0966 protein, complete cds /cds=(-166,3564) /gb=AB023183	36089_at

						/gi=4589575 /ug=Hs.52463 /len=4924	
SYNE-1B(synaptic nuclear envelope 1)	AB018339	Hs.8182			6	Cluster Incl. AB018339:Homo sapiens mRNA for KIAA0796 protein, partial cds /cds=(0,3243) /gb=AB018339 /gi=3882312 /ug=Hs.8182 /len=3900	38113_at
MSF (MLL septin-like fusion)	AB023208	Hs.181002		NM_006640	17q25	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	41220_at
BCL2 (B-cell CLL/lymphoma 2)	M14745	Hs.79241		NM_000633	18q21.3	M14745 /FEATURE= /DEFINITION=HUMBCL2C Human bcl-2 mRNA	1909_at
E2F5 (E2F transcription factor 5, p130-binding)	U31556	Hs.2331		NM_001951	8p22-q21.3	Cluster Incl. U31556:Human transcription factor E2F-5 mRNA, complete cds /cds=(38,1075) /gb=U31556 /gi=939728 /ug=Hs.2331 /len=1728	41275_at

E2F5 (E2F transcription factor 5, p130-binding)	U31556	Hs.2331	NM_001951	8p22-q21.3	U31556 /DEFINITION=HSU31556 transcription factor E2F-5 mRNA, complete cds	1044_s_at
IL4R (interleukin 4 receptor)	X52425	Hs.75545	NM_000418	16p11.2-12.1	X52425 /DEFINITION=HSIL4R Human IL-4-R mRNA for the interleukin 4 receptor	404_at
TLK1 (tousled-like kinase 1)	D50927	Hs.18895	NM_012290	8p22-p12	Cluster Incl. D50927:Human mRNA for KIAA0137 gene, complete cds /cds=(1088,2737) /gb=D50927 /gi=1469196 /ug=Hs.18895 /len=4454	32219_at
MMP9 (matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase))	J05070	Hs.151738	NM_004994	20q11.2-q13.1	Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334	31859_at
SH3BP5 (SH3-domain binding protein 5 (BTK- associated))	AB005047	Hs.109150	NM_004844	1q43	Cluster Incl. AB005047:Homo sapiens mRNA for SH3 binding protein, complete cds /cds=(63,1340) /gb=AB005047	38968_at

						/gi=3116213 /ug=Hs.108150 /len=2570	
GGA2(Golgi-associated, gamma-adaptin ear containing, ARF-binding protein 2	AB029003	Hs.155546	NM_015044	16		Cluster Incl. AB029003:Homo sapiens mRNA for KIAA1080 protein, partial cds /cds=(0,1554) /gb=AB029003 /gi=5689496 /ug=Hs.155546 /len=4791	40278_at
SGP28(specific granule protein (28 kDa); cysteine-rich secretory protein-3)	X94323	Hs.54431	NM_006061	6		Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213612 /ug=Hs.54431 /len=2124	36454_at
KIAA0430(KIAA0430 gene product)	AB007890			16		Cluster Incl. AB007890:Homo sapiens KIAA0430 mRNA, complete cds /cds=(0,3172) /gb=AB007890 /gi=2887438 /ug=Hs.166163 /len=6011	31936_s_at
	U92981					Cluster Incl. U92981:Homo sapiens clone DT1P1B6 mRNA, CAG repeat region /cds=UNKNOWN /gb=U92981 /gi=2781399 /ug=Hs.18081 /len=1429	38577_at

E2F5 (E2F transcription factor 5, p130-binding)	U15642	Hs.2331	NM_001951	8p22-q21.3	U15642 /DEFINITION=HSU15642 transcription factor E2F-5 mRNA, complete cds	1639_s_at
ABCA6 (ATP-binding cassette, sub-family A (ABC1), member 6)	A1651024	Hs.15780		17q21	Cluster Inc. A1651024;wa96h06.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2304059 /clone_end=3' /gb=A1651024 /gi=4735003 /ug=Hs.15780 /len=657	35390_at
EZH1 (enhancer of zeste (Drosophila) homolog 1)	AB002386	Hs.194669	NM_001991	17q21.1-q21.3	Cluster Inc. AB002386:Human mRNA for KIA0388 gene, complete cds /cds=(100,2343) /gb=AB002386 /gi=2224716 /ug=Hs.194669 /len=4606	32259_at
CD19 (CD19 antigen)	M28170	Hs.96023	NM_001770	16p11.2	M28170 /DEFINITION=HUMCSPC Human cell surface protein CD19 (CD19) gene, complete cds	1086_g_at
PRDM2 (PR domain containing 2, with ZNF domain)	D45132	Hs.26719	NM_012231	1p36	D45132 /DEFINITION=HUMHOXY1 Homo sapiens	316_g_at

domain)						mRNA for zinc-finger DNA-binding protein, complete cds	
PSCD1 (pleckstrin homology, Sec7 and coiled/coiled domains 1(cytchesin 1))	M85169	Hs.1050	NM_004762	17q25		Cluster Incl. M85169:Human homologue of yeast sec7 mRNA, - complete cds /cds=(69,1265) /gb=M85169 /gi=338001 /ug=Hs.1050 /len=3301	38666_at
KIAA0136(DNA segment, Chr 16, Johns Hopkins University 32, expressed)	D50926	Hs.70359		21q22.13		Cluster Incl. D50926:Human mRNA for KIAA0136 gene, partial cds /cds=(0,2854) /gb=D50926 /gi=1469194 /ug=Hs.70359 /len=4197	36845_at
TGFB3 (transforming growth factor, beta receptor III (betaglycan, 300kD))	L07594	Hs.79059	NM_003243	1p33-p32		L07594 /FEATURE= Human /DEFINITION=HUMTGFB3C transforming growth factor-beta type III receptor (TGF-beta) mRNA, complete cds	1897_at
DKFZP586F2423(hypothetical protein	AL080209	Hs.13659		7		Cluster Incl. AL080209:Homo sapiens mRNA; cDNA DKFZp586F2423 (from clone DKFZp586F2423) /cds=UNKNOWN /gb=AL080209 /gi=5262698 /ug=Hs.13659	39692_at

						/len=4241	
AIM2 (absent in melanoma 2)	AF024714	Hs.105115	NM_004833	1q22	Cluster Incl. AF024714:Homo sapiens interferon-inducible protein (AIM2) mRNA, complete cds /cds=(245,1276) /gb=AF024714 /gi=2558941 /ug=Hs.105115 /len=1485	34439_at	
LCN2 (lipocalin 2 (oncogene 24p3))	A1762213	Hs.204238	NM_005564	9q34	Cluster Incl. A1762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=A1762213 /gi=5177880 /ug=Hs.204238 /len=677	32821_at	
KIAA0922(KIAA0922 protein)	AB023139	Hs.37892	NM_015196	4	Cluster Incl. AB023139:Homo sapiens mRNA for KIAA0922 protein, partial cds /cds=(0,2372) /gb=AB023139 /gi=4589475 /ug=Hs.37892 /len=2505	39929_at	
KIAA0769(KIAA0769 gene product)	AB018312	Hs.18056	NM_014824	11	Cluster Incl. AB018312:Homo sapiens mRNA for KIAA0769 protein, complete cds /cds=(239,2293) /gb=AB018312	32224_at	

						/gi=3882258 /ug=Hs.19056 /len=4326	
KIAA0746(KIAA0746 protein)	AB018289	Hs.49500		4		Cluster Incl. AB018289:Homo sapiens mRNA for KIAA0746 protein, partial cds /cds=(0,3091) /gb=AB018289 /gi=3882212 /ug=Hs.49500 /len=4086	41585_at
FCER2 (Fc fragment of IgE, low affinity II, receptor for (CD23A))	M15059	Hs.1416	NM_002002	19p13.3		Cluster Incl. M15059:Human Fc-epsilon receptor (IgE receptor) mRNA, complete cds (H107 epitope) /cds=(213,1178) /gb=M15059 /gi=182447 /ug=Hs.1416 /len=1530	34960_q_at
AKAP11 (A kinase (PRKA) anchor protein 11)	AB014529	Hs.232076	NM_016248	13q12.2-13q14.3		Cluster Incl. AB014529:Homo sapiens mRNA for KIAA0629 protein, partial cds /cds=(0,1840) /gb=AB014529 /gi=3327071 /ug=Hs.232076 /len=5883	34857_at
KIAA0543(KIAA0543 protein)	AB011115	Hs.98507		7		Cluster Incl. AB011115:Homo sapiens mRNA for KIAA0543 protein, partial cds /cds=(0,3336) /gb=AB011115 /gi=3043609	41077_at

						/ug=Hs.98507 /len=6443			
PIR121(p53 inducible protein)	L47738	Hs.258503			5	Cluster Incl. L47738:Homo sapiens inducible protein mRNA, complete cds /cds=(1004,1714) /gb=L47738 /gi=1009098 /ug=Hs.80313 /len=2881			37579_at
MAP3K5 (mitogen-activated protein kinase kinase kinase 5)	U67156	Hs.151988		NM_005923	6q22.33	U67156 /FEATURE= Human /DEFINITION=HSU67156 mitogen-activated kinase kinase kinase 5 (MAPKKK5) mRNA, complete cds			1327_s_at
FLJ22531(hypothetical protein FLJ22531)	W80358	Hs.55613		NM_024650	11	Cluster Incl. W80358:zh49a07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-415380 /clone_end=3 /gb=W80358 /gi=1391395 /ug=Hs.55613 /len=547			41804_at
MGEA5 (meningioma expressed antigen 5 (hyaluronidase))	AB014579	Hs.5734		NM_012215	10q24.1-q24.3	Cluster Incl. AB014579:Homo sapiens mRNA for KIAA0679 protein, partial cds /cds=(0,2303) /gb=AB014579 /gi=3327171 /ug=Hs.5734 /len=4303			35317_at

MDS019(phorbolin-like protein MDS019)	AL078641	Hs.250619	NM_021822	22	Cluster Incl. AL078641:Human DNA sequence from clone 494G10 on chromosome 22 Contains part of a gene similar to phorbolin 2, ESTs and a GSS /cds=(0,419) /gb=AL078641 /gi=5162948 /ug=Hs.112449 /len=751	41472_at
KIAA0240(KIAA0240 protein)	D87077	Hs.196275		6	Cluster Incl. D87077:Human mRNA for KIAA0240 gene, partial cds /cds=(0,2953) /gb=D87077 /gi=1510154 /ug=Hs.196275 /len=6060	38892_at
PRKCB1 (protein kinase C, beta 1)	X07109	Hs.77202	NM_002738	16p11.2	X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase C (PKC) type beta II /NOTE=replacement of probe set 1216_at	160029_at
CCR7 (chemokine (C-C motif) receptor 7)	L31584	Hs.1652	NM_001838	17q12-q21.2	L31584 /FEATURE=exon /DEFINITION=HUMEBI103 Human G protein-coupled receptor (EBI 1) gene exon 3, complete cds	1097_s_at

CDC25B (cell division cycle 25B)	S78187	Hs.153752	NM_004358	20p13	S78187 /DEFINITION=S78187 CDC25Hu2=cdc25+ homolog [human, mRNA, 3118 nt]	/FEATURE= 1347_at
CCR2 (chemokine (C-C motif) receptor 2)	U95626	Hs.395	NM_000647	3p21	Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607	37149_s_at
	AL049701				Cluster Incl. AL049701:Human gene from PAC 433G19, chromosome 1 /cds=(0,370) /gb=AL049701 /gi=4678835 /ug=Hs.107325 /len=648	34446_at
P2Y10(putative purinergic receptor)	AF000545	Hs.296433	NM_014499	X	AF000545 /DEFINITION=HSAF000545 Homo sapiens putative purinergic receptor P2Y10 gene, complete cds	358_at

MGC12335(hypothetical protein MGC12335)	AL022724	Hs.97411	NM_032744	6	Cluster Incl. AL022724:Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs /cds=(94,861) /gb=AL022724 /gi=4468306 /lug=Hs.97411 /len=1037	34043_at
P2Y10(putative purinergic receptor)	Z82200	Hs.296433	NM_014499	X	Cluster Incl. Z82200:Human DNA sequence from clone 333E23 on chromosome Xq21.1 Contains putative purinergic receptor P2Y10 /cds=(0,1019) /gb=Z82200 /gi=2370075 /lug=Hs.166137 /len=1020	36413_at
IFI41 (interferon-induced protein 41, 30KD)	L22342	Hs.241510	NM_004509		Cluster Incl. L22342:Human nuclear phosphoprotein mRNA, complete cds /cds=(0,746) /gb=L22342 /gi=402204 /lug=Hs.38125 /len=835	35718_at
ARH1 (ras homolog gene family, member H)	Z35227	Hs.109918	NM_004310	4p13	Cluster Incl. Z35227:H.sepiens TTF mRNA for small G protein /cds=(579,1154)	37416_at

						/gb=Z35227 /gj=609016 /ug=Hs.109918 /len=1427			
PRKCB1 (protein kinase C, beta 1)	X07109	Hs.77202	NM_002738	16p11.2	X07109	/FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase C (PKC) type beta II	1217_g_at		
	AL049471				Cluster Incl. AL049471:Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012) /cds=UNKNOWN /gb=AL049471 /gj=4500266 /ug=Hs.12702 /len=2905		41690_at		
KCNN4 (potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4)	AF022797	Hs.10082	NM_002250	19q13.2	Cluster Incl. AF022797:Homo sapiens intermediate conductance calcium- activated potassium channel (hKCa4) mRNA, complete cds /cds=(396,1679) /gb=AF022797 /gj=2674355 /ug=Hs.10082 /len=2238		41106_at		

USF2 (upstream transcription factor 2, c-fos interacting)	AD000684	Hs.93649	NM_003367	19q13	Cluster Incl. AD000684:Homo sapiens DNA from chromosome 19-cosmid R30879 containing USF2, genomic sequence /cds=(0,1290) /gb=AD000684 /gi=1905917 /ug=Hs.95697 /len=1291	38324_at
KIAA0471(KIAA0471 gene product)	AB007940			1	Cluster Incl. AB007940:Homo sapiens mRNA for KIAA0471 protein, complete cds /cds=(412,1524) /gb=AB007940 /gi=3413903 /ug=Hs.107325 /len=6634	34445_at
SLC23A1 (solute carrier family 23 (nucleobase transporters), member 1)	D87075	Hs.82042	NM_005116	20p13	Cluster Incl. D87075:Human mRNA for KIAA0238 gene, partial cds /cds=(0,992) /gb=D87075 /gi=1510150 /ug=Hs.82042 /len=5608	38122_at
KIAA0441(KIAA0441 gene product)	AB007901				Cluster Incl. AB007901:Homo sapiens KIAA0441 mRNA, complete cds /cds=(168,2261) /gb=AB007901 /gi=2662162 /ug=Hs.32511 /len=5597	39658_at

					6	Cluster Incl. X07203:Human mRNA for CD20 receptor (S7) /cds=(90,983) /gb=X07203 /gi=29775 /ug=Hs.89751 /len=1597	40749_at
LEF1 (lymphoid enhancer-binding factor 1)	AL049409	Hs.44865	NM_016269	4q23-q25		Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419	38021_at
TCL1A (T-cell leukemia/lymphoma 1A)	X82240	Hs.2484	NM_021966	14q32.1		Cluster Incl. X82240:H.sapiens mRNA for Tcell leukemia/lymphoma 1 /cds=(45,389) /gb=X82240 /gi=624960 /ug=Hs.2484 /len=1312	39318_at
SCAP1 (src family associated phosphoprotein 1)	Y11215	Hs.19126	NM_003726	17q21.3		Cluster Incl. Y11215:Homo sapiens mRNA for SKAP55 protein /cds=(70,1149) /gb=Y11215 /gi=2252495 /ug=Hs.19126 /len=1524	38862_at

NCOA1 (nuclear receptor coactivator 1)	U59302	Hs.74002	NM_003743	2p23	U59302 /DEFINITION=HSU59302 Human steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds	484_at
TRAF1 (TNF receptor-associated factor 1)	U19261	Hs.2134	NM_005658	9q33-q34	U19261 /DEFINITION=HSU19261 Homo sapiens Epstein-Barr virus-induced protein mRNA, complete cds	849_g_at
KIAA0239(KIAA0239 protein)	D87076	Hs.9729	NM_015288	5	Cluster Incl. D87076:Human mRNA for KIAA0239 gene, partial cds /cds=(0,1716) /gb=D87076 /gj=1510152 /ug=Hs.9729 /len=5630	38342_at
CASK (calcium/calmodulin-dependent serine protein kinase (MAGUK family))	AF035582	Hs.151469	NM_003888	xp11.4	Cluster Incl. AF035582:Homo sapiens CASK mRNA, complete cds /cds=(15,2708) /gb=AF035582 /gj=2661105 /ug=Hs.151469 /len=3919	31854_at
KIAA0053(KIAA0053 gene product)	D29642	Hs.1528	NM_014882	2	Cluster Incl. D29642:Human mRNA for KIAA0053 gene, complete cds	38149_at

						/cds=(193,2109) /gb=D29642 /gi=473934 /ug=Hs.1528 /len=2739				
APOC4 (apolipoprotein C-IV)	U32576	Hs.110675	NM_001646	19q13.2	Cluster Incl. U32576:Human apolipoprotein apoC-IV (APOC4) gene, complete cds /cds=(40,423) /gb=U32576 /gi=975892 /ug=Hs.110675 /len=613	34454_r_at				
SP100 (nuclear antigen Sp100)	M60618	Hs.77617	NM_003113	2q37.1	Cluster Incl. M60618:Human nuclear autoantigen (SP-100) mRNA, complete cds /cds=(31,1473) /gb=M60618 /gi=178688 /ug=Hs.77617 /len=1879	37352_at				
KIAA1010(KIAA1010 protein)	AB023227	Hs.23860		10	Cluster Incl. AB023227:Homo sapiens mRNA for KIAA1010 protein, partial cds /cds=(0,3949) /gb=AB023227 /gi=4589669 /ug=Hs.23860 /len=5524	34712_at				
SP100 (nuclear antigen Sp100)	M60618	Hs.77617	NM_003113	2q37.1	Cluster Incl. M60618:Human nuclear autoantigen (SP-100) mRNA, complete cds /cds=(31,1473) /gb=M60618	37353_g_at				

						/gi=178688 /ug=Hs.77617 /len=1879	
JAK1 (Janus kinase 1 (a protein tyrosine kinase))	AL039831	Hs.50651	NM_002227	1p32.3-p31.3	Cluster Incl. AL039831:DKFZp434D1112_s1 sapiens cDNA, 3 end /clone=DKFZp434D1112 /clone_end=3 /gb=AL039831 /gi=5868713 /ug=Hs.50651 /len=579	34877_at	
PPP3CC (protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma))	S46622	Hs.75206	NM_005605	8	Cluster Incl. S46622:calcineurin A catalytic subunit [human, testis, mRNA, 2134 nt] /cds=(286,1794) /gb=S46622 /gi=258000 /ug=Hs.75206 /len=2134	32541_at	
MTMR1 (myotubularin related protein 1)	AJ224979	Hs.23200		xq28	Cluster Incl. AJ224979:Homo sapiens mRNA for MTMR1 protein /cds=(0,1990) /gb=AJ224979 /gi=4128155 /ug=Hs.23200 /len=2582	34654_at	
HLA-F (major histocompatibility complex, class I, F)	AL022723	Hs.110309	NM_018950	6p21.3	Cluster Incl. AL022723:dJ377H14.9 (major histocompatibility complex, class I, F (CDA12)) /cds=(97,1185) /gb=AL022723	37420_i_at	

						/gi=5002624 /ug=Hs.110309 /len=1303	
PRKCB1 (protein kinase C, beta 1)	X06318	Hs.77202	NM_002738	16p11.2	X06318	/FEATURE=cds /DEFINITION=HSPKCB1A Human mRNA for protein kinase C (PKC) type beta I	1336_s_at
GTSE1 (G-2 and S-phase expressed 1)	AL031588	Hs.122552	NM_016426	22q13.2-q13.3	Cluster Incl. AL031588.dJ1163J1.3 (novel protein similar to mouse B99) /cds=(0,2140) /gb=AL031588 /gi=4007108 /ug=Hs.122552 /len=2821		39872_at
SLC7A6 (solute carrier family 7 (cationic amino acid transporter, y+ system), member 6)	D87432	Hs.10315	NM_003983	16q22.1-q22.3	Cluster Incl. D87432:Human mRNA for KIAA0245 gene, complete cds /cds=(261,1806) /gb=D87432 /gi=1665758 /ug=Hs.10315 /len=6296		39533_at

Table 16: Major Types (BM, CLL, CML, ALL, AML)

HAUPTGRUPPEN

COMPARISON		Description				
CLL - CML		M12886 /FEATURE= /DEFINITION=HUMTCBYY Human T-cell receptor active beta-chain mRNA, complete cds	HG_U95_Target: 1105_s_at_HG- U95Av2	T cell receptor beta locus	TRB	7q35
AML - CML		Cluster Incl. AL036554:DKFZp564J2262_r1 Homo sapiens cDNA 5' end; clone=DKFZp564J2262 /clone_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.137931793 /len=517	HG_U95_Target: 31793_at_HG- U95Av2	defensin, alpha 3, neutrophil-specific	DEFA3	8pter-p23.3
AML - BM	ALL - BM	Cluster Incl. AB006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=(256,1212) /gb=AB006746 /gi=3510298 /ug=Hs.198282 /len=2077	HG_U95_Target: 32775_r_at_HG- U95Av2	phospholipid scramblase 1	PLSCR1	3q23

AML - CML	Cluster Incl. A1762213:wi54d04.x1 Homo sapiens cDNA, 3' end /cds=IMAGE2394055 /cds_end=3 /gb=A1762213 /gi=5177680 /ug=Hs.204238 /len=677	HG_U95_Target 32821_at_HG- U95AV2	32821_at	lipocalin 2 (oncogene 24p3)	LCN2	9q34
ALL - BM	Cluster Incl. AB007931:Homo sapiens mRNA for KIAA0462 protein, partial cds /cds=(0,6831) /gb=AB007931 /gi=3413885 /ug=Hs.239686 /len=7150	HG_U95_Target 33860_at_HG- U95AV2	33860_at	KIAA0462 protein	KIAA0462*	1p36.13
ALL - AML	Cluster Incl. S60099:APPH=amyloid precursor protein homolog [human, placenta, mRNA, 3727 nt] /cds=(72,2363) /gb=S60099 /gi=300168 /ug=Hs.6479733944_at_HG- U95AV2 /len=3727	HG_U95_Target 33944_at_HG- U95AV2	33944_at	amyloid beta (A4) precursor-like protein 2	APLP2	11q24
ALL - AML	Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409 /gi=450019436021_at_HG- U95AV2 /ug=Hs.44865 /len=1419	HG_U95_Target 36021_at_HG- U95AV2	36021_at	lymphoid enhancer-binding factor 1	LEF1	4q23-q25
AML - CLL	Cluster Incl. Z49194:H.sapiens mRNA for oct-binding factor /cds=(523,1293) /gb=Z49194 /gi=974830 /ug=Hs.2407 /len=3301	HG_U95_Target 36239_at_HG- U95AV2	36239_at	POU domain, class 2, associating factor 1	POU2AF1	11q23.1
AML - CML	Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213612 /ug=Hs.54431 /len=2124	HG_U95_Target 36464_at_HG- U95AV2	36464_at	specific granule protein (28 kDa)	SGP28*	6p12.3

			U95AV2				
AML - BM		Cluster Incl. Z38026: Haeplens mRNA for FALL-39 peptide antibiotic (cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	HG_U95_Target: 36710_at_HG- U95AV2	36710_at	cathelidin antimicrobial peptide	CAMP	3p21.3
ALL - CML		Cluster Incl. L01664: Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds (cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586	HG_U95_Target: 36809_at_HG- U95AV2	36809_at	Charot-Leyden crystal protein	CLC	19q13.1
ALL - AML		Cluster Incl. U41635: Human OS-9 precursor mRNA, complete cds (cds=(85,2088) /gb=U41635 /gi=1322233 /ug=Hs.76228 /len=2736	HG_U95_Target: 36996_at_HG- U95AV2	36996_at	amplified in osteosarcoma	OS-9*	12q13
ALL - CML		Cluster Incl. AF010400: untitled (cds=(50,1063) /gb=AF010400 /gi=2612878 /ug=Hs.77290 /len=1242	HG_U95_Target: 37311_at_HG- U95AV2	37311_at	transaldolase 1	TALDO1	11p15.5-p15.4
BM - CML		Cluster Incl. U52682: Human lymphocyte specific interferon regulatory factor/interferon regulatory factor 4 (LSIRF/IRF4) mRNA, complete cds (cds=(125,1477) /gb=U52682 /gi=1376108 /ug=Hs.82132 /len=5320	HG_U95_Target: 37625_at_HG- U95AV2	37625_at	Interferon regulatory factor 4	IRF4	6p25-p23

BM - CLL	Cluster Incl. AB023169: Homo sapiens mRNA for KIAA0952 protein, complete cds (cds=(359,1927) /gb=AB023169 /gi=4589547 /ug=Hs.7935 /len=4856	HG_U95_Target: 37755_at_HG- U95AV2	37755_at	KIAA0952 protein	KIAA0952	20p12.1
ALL - CLL	Cluster Incl. U92981: Homo sapiens clone DT1P186 mRNA, CAG repeat region (cds=UNKNOWN /gb=U92981 /gi=2781399 /ug=Hs.18081 /len=1429	HG_U95_Target: 38577_at_HG- U95AV2	38577_at	unknown	Unknown*	unknown
AML - CLL	Cluster Incl. M63928: Homo sapiens T cell activation antigen (CD27) mRNA, complete cds (cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204	HG_U95_Target: 38578_at_HG- U95AV2	38578_at	tumor necrosis factor receptor superfamily, member 7	TNFRSF7	12p13
ALL - BM	Cluster Incl. U04270: Human putative potassium channel subunit (h-erg) mRNA, complete cds (cds=(183,3662) /gb=U04270 /gi=487737 /ug=Hs.18802 /len=4070	HG_U95_Target: 38858_at_HG- U95AV2	38858_at	potassium voltage-gated channel, subfamily H (eag-related), member 2	KCNH2	7q35-q38
ALL - AML	Cluster Incl. AL008726.dJ337O18.2 (Lysosomal Protective Protein precursor (ECH3.4.18.5, Cathepsin A, Carboxypeptidase C)) (cds=(133,1575) /gb=AL00872639062 /gi=3183870 /ug=Hs.118126 /len=1946	HG_U95_Target: 39062_at_HG- U95AV2	39062_at	protective protein for beta-galactosidase (galactosialidosis)	PPGB	20q13.1
BM - CLL	Cluster Incl. U03057: Human actin bundling protein (HSN) mRNA, complete cds (cds=(111,1592) /gb=U03057 /gi=458027 /ug=Hs.118400 /len=2767	HG_U95_Target: 39070_at_HG-	39070_at	singed (Drosophila)-like (sea urchin fascin homolog like)	SNL	7p22

			U95AV2					
ALL - AML		Cluster Incl. AB023208: Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	HG_U95_Target 41220_at_HG- U95AV2	41220_at	MLL septin-like fusion	MSF	17q25	
CLL - CML	BM - CML	Cluster Incl. U15085: Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162 /len=1362	HG_U95_Target 41609_at_HG- U95AV2	41609_at	major histocompatibility complex, class II, DM beta	HLA-DMB	6p21.3	
ALL - CLL		U59302 /FEATURE= /DEFINITION=HSU59302 Human steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds	HG_U95_Target 484_at_HG- U95AV2	484_at	nuclear receptor coactivator 1	NCOA1	2p23	
		description	HG-U95_Target	Probe Set ID	Title	Gene Symbol	Map Location	

Table 17. AML_WHO [other, t(11q23)/MLL, t(8;21), inv(16), t(15;17)]

INV16-	INV16-OTHER	INV16-T821	Cluster Incl. AF013570: Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944 /ug=Hs.78344 /len=2580	HG_U85_Target:37407_s_at_HG-U85AV2	37407_s_at	myosin, heavy polypeptide 11, smooth muscle	MYH11	16p13.13-p13.12
INV16-			AF001548 /FEATURE=mRNA /DEFINITION=HUA01548 Human chromosome 16 BAC clone CIT987SK-A1_HG-U85AV2 815A9, complete sequence	HG_U85_Target:787_s_at_HG-U85AV2	787_at	myosin, heavy polypeptide 11, smooth muscle	MYH11	16p13.13-p13.12
INV16-OTHER			Cluster Incl. U68186: Human extracellular matrix protein 1 mRNA, complete cds /cds=(103,1725) /gb=U68186 /gi=2660883 /ug=Hs.81071 /len=1819	HG_U85_Target:37600_s_at_HG-U85AV2	37600_at	extracellular matrix protein 1	ECM1	1q21

INV16-T1517					M25280 /DEFINITION=HUMLNHR Human lymph node homing receptor mRNA, complete cds	HG_U95_Target:245_at_HG-U95AV2	245_at	selectin L (lymphocyte adhesion molecule 1)	SELL	1q23-q25
INV16-T1517					Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048	HG_U95_Target:38833_at_HG-U95AV2	38833_at	major histocompatibility complex, class II, DP alpha 1	HLA-DPA1	6p21.3
INV16-T821					Cluster Incl. AF008484:Homo sapiens putative oral tumor suppressor protein (doc-1) mRNA, complete cds /cds=(522,869) /gb=AF008484 /gi=2738496 /ug=Hs.3436 /len=1608	HG_U95_Target:41535_at_HG-U95AV2	41535_at	CDK2-associated protein 1	CDK2AP1	12q24.31
MLL-					Cluster Incl. AB007888:Homo sapiens KIAA0428 mRNA, complete cds /cds=(1414,2526) /gb=AB007888 /ug=Hs.28578 /len=5940	HG_U95_Target:34306_at_HG-U95AV2	34306_at	muscleblind (Drosophila)-like	MBNL	3q25
MLL-	MLL-T821				Cluster Incl. X71129:H.sapiens mRNA for electron transfer flavoprotein beta subunit /cds=(27,794) /gb=X71129 /gi=297901	HG_U95_Target:36881_at_HG-U95AV2	36881_at	electron-transfer-flavoprotein, beta polypeptide	ETFB	19q13.3

[illegible]

MLL-OTHER				Cluster Incl. U03105:Human B4-2 protein mRNA complete cds /cds=(113,1095) /hg_U05_Target:36980 /gb=U03105 /gi=476094 /ug=Hs.75969_at_HG-U05AV2 /len=2061	36980_at	proline-rich protein with nuclear targeting signal	B4-2*	6q16.1
MLL-OTHER				Cluster Incl. AF001461: Homo sapiens Kruppel-like zinc finger protein Zf9 mRNA /hg_U05_Target:37026 complete cds /cds=(30,881) /gb=AF001461_at_HG-U05AV2 /gi=3378030 /ug=Hs.76526 /len=1354	37026_at	core promoter element binding protein	COPEB	10p15
MLL-OTHER				Cluster Incl. M36542: Human lymphoid-specific transcription factor mRNA, complete cds /cds=(54,1445) /gb=M36542 /gi=339495 /ug=Hs.1101 /len=2048	37417_at	POU domain, class 2, transcription factor 2	POU2F2	19q13.31
MLL-T1517				Cluster Incl. U25182: Human antioxidant enzyme AOE37-2 mRNA, complete cds /cds=(43,858) /gb=U25182 /gi=799380 /ug=Hs.83383 /len=921	38435_at	peroxiredoxin 4	PRDX4	Xp22.13
MLL-T1517	OTHER-T1517	T1517-	T1517-T821	Cluster Incl. X78817: Homo sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817	39649_at	Rho GTPase activating protein 4	ARHGAP4	Xq28

[illegible]

T1517-				Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /HG_U85_Target:38487 /gb=D87433 /gl=1665760 /ug=Hs.84753_at_HG-U85AV2 /len=6777	38487_at	hypothetical protein FLJ12442, KIAA0246	STAB1*	3p21.31
T821-				Cluster Incl. AF045229: Homo sapiens regulator of G protein signaling 10 mRNA /HG_U85_Target:33121 /cds=(132,635) /gb=AF045229_g_at_HG-U85AV2 /gl=2806029 /ug=Hs.82280 /len=753	33121_g_at	regulator of G-protein signalling 10	RGS10	10q25
T821-				Cluster Incl. D43638: Human mRNA for MTG8a protein, complete cds /HG_U85_Target:35638 /cds=(411,2144) /gb=D43638 /gl=940399_at_HG-U85AV2 /ug=Hs.31551 /len=3460	35638_at	core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related	CBFA2T1	8q22
T821-				Cluster Incl. X64624: H.sapiens mRNA for RDC-1 POU domain containing protein /HG_U85_Target:35940 /cds=(277,1272) /gb=X64624 /gl=35914_at_HG-U85AV2 /ug=Hs.211588 /len=3492	35940_at	POU domain, class 4, transcription factor 1	POU4F1	13q21.1-q22
used in comparison				Description	HG-U85 Target	Title	Gene Symbol	Map Location

Table 17. Hierarchical clustering of 55 AML samples (rows) versus 25 informative genes (columns). In total, 15 comparisons within the 5 groups were performed (pairwise and one-versus-all). Genes were selected for maximal accuracy and confidence based on a modified signal-to-noise (S2N) algorithm [see (Ref)]. The scaled gene expression levels are coded by intensity and shown on a scale from black (no gene expression) to bright red (highest expression). The AML subgroups 'other' (n=10), t(11q23)/MLL (n=10), inv(16) (n=10), t(8;21) (n=9), and t(15;17) (n=16) are colored according to their chromosomal aberrations. The minimal set of informative genes is given by approved symbols by the HGNC (not yet approved genes are marked by asterisks).

Table 18. ALL_détail [t(11q23)/MLL, t(9;22), t(8;14), T-ALL]

ALLPH-ALLT	M12888 /FEATURE= /DEFINITION=HUMTCBY Human T-cell receptor active beta-chain mRNA, complete cds	HG_U95_Target:1105_s_at_HG-U95AV2	1105_s_at	T cell receptor beta locus	TRB	7q35
ALLPH-	U03779 /FEATURE=mRNA /DEFINITION=HUMCALLA Human common acute lymphoblastic leukemia antigen (CALLA) mRNA, complete cds	HG_U95_Target:1389_at_HG-U95AV2	1389_at	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	MME	3q25.1-q25.2
ALL814-	M16038 /FEATURE= /DEFINITION=HUMLYN Human lymphoma tyrosine kinase mRNA encoding a tyrosine kinase	HG_U95_Target:1402_at_HG-U95AV2	1402_at	v-src-1 Yamaguchi sarcoma viral related oncogene homolog	LYN	8q13
ALL814-ALLMLL	U22376 /FEATURE=cds#3 /DEFINITION=HSU22376 Human (c-myb) gene, complete primary cds, and five complete alternatively spliced cds	HG_U95_Target:1474_s_at_HG-U95AV2	1474_s_at	v-myb myeloblastosis viral oncogene homolog (avian)	MYB	6q22-q23
ALL814-ALLMLL	M15024 /FEATURE= /DEFINITION=HUMCMYBLA Human c-myb mRNA, complete cds	HG_U95_Target:2042_s_at_HG-U95AV2	2042_s_at	v-myb avian myeloblastosis viral oncogene homolog	MYB	6q22-q23

ALLMLL-ALLT	123805 /FEATURE= /DEFINITION=HUMCATENIN Human alpha1(E)-catenin mRNA, complete cds	HG_U95_Target:2069 s_at_HG-U95AV2	2069_s_at	CTNNA1 catenin (cadherin-associated protein), alpha 1 (102kD)	5q31
ALLT-	Cluster Incl. AL034374:Human DNA sequence from clone 4B3K16 on chromosome 6p12.1-21.1. Contains (parts of) two novel genes, 40S Ribosomal protein S16 and 60S Ribosomal protein L31 pseudogenes, ESTs, STSs, GSSs and a putative CpG island /cds=(0,703) /gb=AL034374 /gi=44555665 /ug=Hs.234655 /len=2432	HG_U95_Target:3382 s_at_HG-U95AV2	3382_s_at	HELO1 homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	6
ALL814-ALLPH	Cluster Incl. AB020674:Homo sapiens mRNA for KIAA0867 protein, complete cds /cds=(152,1732) /gb=AB020674 /gi=4240222 /ug=Hs.52081 /len=4339	HG_U95_Target:3526 s_at_HG-U95AV2	3526_s_at	MONDOA* KIAA0867 protein	12q21.31
ALL814-ALLT	Cluster Incl. D90144:Homo sapiens gene for LD78 alpha precursor, complete cds /cds=(86,364) /gb=D90144 /gi=219905 /ug=Hs.73817 /len=781	HG_U95_Target:3610 s_at_HG-U95AV2	3610_s_at	SCYA3 small inducible cytokine A3 (homologous to mouse Mip-1a)	17q11-q21
ALLMLL-	Cluster Incl. X78947:H.sapiens mRNA for connective tissue growth factor /cds=(145,1194) /gb=X78947 /gi=474933 /ug=Hs.75511 /len=2312	HG_U95_Target:3663 s_at_HG-U95AV2	3663_s_at	CTGF connective tissue growth factor	6q23.1

ALLMLL-	Cluster Incl. D16532:Human gene for very low density lipoprotein receptor, 5flanking and /cds=(615,3236) /gb=D16532 /gi=407220 /ug=Hs.73728 /len=3853	HG_U95_Target:3687 3_at_HG-U95AV2	36873_at	very low density lipoprotein receptor	VLDLR	9p24
ALL814-	Cluster Incl. U05770:Human annexin V (ANX5) gene /cds=(164,1126) /gb=U05770 /gi=2182176 /ug=Hs.78274 /len=1597	HG_U95_Target:3774 7_at_HG-U95AV2	37747_at	annexin A5	ANXA5	4q28-q32
ALLPH-ALLT	Cluster Incl. AA919102:c184h02.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-1536339 /clone_end=3 /gb=AA919102 /gi=3058992 /ug=Hs.95327 /len=622	HG_U95_Target:3831 9_at_HG-U95AV2	38319_at	CD3D antigen, delta polypeptide (HT3 complex)	CD3D	11q23
ALLMLL-ALLPH	Cluster Incl. AJ010059:Homo sapiens . SIT protein /cds=(87,677) /gb=AJ010059 /gi=4888891 /ug=Hs.88012 /len=1232	HG_U95_Target:4072 3_at_HG-U95AV2	40723_at	SHP2 interacting transmembrane adaptor	SIT*	9p13-p12
ALLMLL-ALLT	Cluster Incl. AF-102803:unlabeled /cds=(2,2722) /gb=AF-102803 /gi=4092760 /ug=Hs.178452 /len=3668	HG_U95_Target:4115 3_f_at_HG-U95AV2	41153_f_at	catenin (cadherin-associated protein), alpha 1 (102KD)	CTNNA1	5q31
ALL814-ALLPH	Cluster Incl. AW024285:w659d06.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2512715 /clone_end=3 /gb=AW024285 /gi=5877815 /ug=Hs.179882 /len=550	HG_U95_Target:4117 7_at_HG-U95AV2	41177_at	hypothetical protein FLJ12443	FLJ12443*	5p15.33

ALLB14-ALLT	Cluster Incl. X02894:Human mRNA for adenosine deaminase (adenosine aminohydrolase, EC 3.5.4.4) /gb=X02894 /gi=28379 /ug=Hs.12174_at_HG-U95AV2 /len=1498	HG_U95_Target:4155 4164_at	adenosine deaminase	ADA	20q12-q13.11
ALLPH-	Cluster Incl. AB020677: Homo sapiens mRNA for KIAA0870 protein, complete cds /cds=(435,1998) /gb=AB020677 /gi=4240228 /ug=Hs.18166 /len=4484	HG_U95_Target:4173 41734_at	KIAA0870 protein	KIAA0870*	8q24.3
ALLMIL-ALLPH	Glucocorticoid Receptor, Beta	HG_U95_Target:706 706_at	Glucocorticoid Receptor, Beta		
used in comparison	Description_Affymetrix	HG-U95 Target	Title	Gene Symbol	Map Location

Table 18. Hierarchical clustering of 17 ALL samples (rows) versus 19 informative genes (columns). In total, 10 pairwise or OVA comparisons within the 4 groups were performed. Genes were selected for maximal accuracy and confidence based on a modified

S2N algorithm [see (Ref)]. The scaled gene expression levels are coded by intensity and shown on a scale from black (no gene expression) to bright red (highest expression). The ALL subgroups t(11q23)/MLL (n=4), t(9;22) (n=7), t(8;14) (n=3), and T-ALL (n=3) are colored according to their chromosomal aberrations. The minimal set of informative genes is given by approved symbols by the HGNC (asterisks mark not yet approved genes).

Table 19 - Additional Comparisons

ALLPHNEG - ALLPHPOS						
38336_at	Cluster Incl. AB023230:Homo sapiens mRNA for KIAA1013 protein, partial cds /cds=(0,3188) /gb=AB023230 /gi=4588675 /ug=Hs.96427 /len=4783	HG_U95_Target:38336_at_HG-U95AV2	38336_at	KIAA1013 protein	KIAA1013	3
33134_at	Cluster Incl. AB011083:Homo sapiens mRNA for KIAA0511 protein, partial cds /cds=(0,2802) /gb=AB011083 /gi=3043545 /ug=Hs.8402 /len=3563	HG_U95_Target:33134_at_HG-U95AV2	33134_at	adenylate cyclase 3	ADCY3	2p24-p22

ALLB - ALLT						
38319_at	Cluster Incl. AA919102:cl94h02.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-1536339 /clone_end=3 /gb=AA919102 /gi=3058992 /ug=Hs.95327 /len=622	HG_U95_Target:38319_at_HG-U95AV2	38319_at	CD3D antigen, delta polypeptide (TIT3 complex)	CD3D	11q23

1105_s_at	M12886 /FEATURE= /DEFINITION=HUMTCBYH Human T-cell receptor active beta-chain mRNA, complete cds	HG_U95_Target:1105_s_1105_s_at at_HG-U95AV2	T cell receptor beta locus	TRB	7q35
ALLPH - CML					
38894_g_at	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial) ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gl=3136	HG_U95_Target:38894_38894_g_at at_HG-U95AV2	Cluster	AL008637	unknown
35016_at	Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cds=(785,1493) /gb=M13560 /gl=184518 /ug=Hs.84298 /len=2080	HG_U95_Target:35016_35016_at at_HG-U95AV2	CD74 antigen (invariant polypeptide of major histocompatibility class II antigen-associated)	CD74	5q32
39301_at	Cluster Incl. X85030:Human spleen mRNA for skeletal muscle-specific calpain /cds=(0,2465) /gb=X85030 /gl=791039 /ug=Hs.239689 /len=2466	HG_U95_Target:39301_39301_at at_HG-U95AV2	calpain 3, (p94)	CAPN3	15q15.1-q21.1

ALLMLL - AMLMLL							
266_s_at	L33930 /FEATURE= /DEFINITION=HUMCD24B Homo sapiens CD24 signal transducer mRNA complete cds and 3' region	HG_U95_Target:266_s_at HG-U95AV2	266_s_at	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	CD24	6q21	
36638_at	Cluster Ind. X78947:H.sapiens mRNA for connective tissue growth factor /cds=(145,1194) /gb=X78947 /gi=474933 /ug=Hs.75511 /len=2312	HG_U95_Target:36638_at HG-U95AV2	36638_at	connective tissue growth factor	CTGF	6q23.1	

WO 03/039443

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PCT/EP02/12303

Table 20

1. Analyse: major leukemia types versus normal bone marrow

ALL - AML		samples: 18 / 59	pValue	selected
<i>accuracy</i>		0.974025974025974		
<i>confidence</i>		0.949191799863432		
1	41220_at	1.43161207339479	0	*
2	36996_at	-1.41523985920205	0	*
3	33944_at	-1.36856428236618	0	*
4	41809_at	1.34726978852919	0	
5	39062_at	-1.32477468024042	0	*
6	36021_at	1.29482788383042	0	*
7	40282_s_at	-1.25276275727203	0	
8	39801_at	-1.18216117554755	0	
9	41808_at	1.16535104461878	0	
10	38791_at	-1.16212420300011	0	

11	38705_at	1.10578452683281	0
12	38017_at	1.09519463190211	0
13	38233_at	-1.08734958364712	0
14	40081_at	-1.06895950257537	0
15	33414_at	-1.06893939139052	0
16	36644_at	-1.06866972901421	0
17	1497_at	-1.05371604908866	0
18	34670_at	-1.0471297974693	0
19	39689_at	-1.02349800799274	0
20	36553_at	0.461827371901751	0

ALL - BM

samples: 18 / 8

accuracy

1

confidence

0.973577941615687

1	32775_r_at	-1.99123472883631	0	*
2	38858_at	-1.89835994048167	0	*
3	33860_at	-1.8349786493313	0	*
4	33944_at	-1.79527299060519	0	

5	32800_at	-1.78206927960542	0
6	35204_at	-1.77698316964481	0
7	38112_g_at	-1.75527325798005	0
8	38735_at	-1.75431905717345	0
9	137_at	-1.75261998994426	0
10	1495_at	-1.73006006400362	0
11	36661_s_at	-1.70636382014738	0
12	38225_at	-1.66016477586249	0
13	39860_at	1.65854625573936	0
14	32166_at	-1.65691236756089	0
15	32530_at	1.64232673980553	0
16	35355_at	1.62316234982832	0
17	1529_at	-1.60938224689727	0
18	36790_at	-1.6093508135706	0
19	2045_s_at	-1.59880026139776	0
20	36553_at	0.997704664996536	0

ALL - CLL

samples: 18 / 8

	<i>accuracy</i>	1	
	<i>confidence</i>	1	
1	484_at	-2.96991037890552	0
2	38577_at	-2.76720679743789	0
3	2019_s_at	-2.66997144118244	0
4	33812_at	-2.65004620998946	0
5	34663_at	-2.56576070575816	0
6	36894_at	-2.56382539311197	0
7	39670_at	-2.48013356223836	0
8	41660_at	-2.4799018378336	0
9	39165_at	-2.3871739157192	0
10	31870_at	-2.36838597731039	0
11	34871_at	-2.36033294682702	0
12	34830_at	-2.33471776306134	0
13	31936_s_at	-2.25951360532653	0
14	1062_g_at	-2.25550068155602	0
15	41847_at	-2.23298915825072	0
16	1217_g_at	-2.21920314115838	0

17	1529_at	-2.17991363072808	0
18	41796_at	-2.17392867117507	0
19	32597_at	-2.13552223797253	0
20	33266_at	1.44232706973843	0

ALL - CML

samples: 18 / 10

accuracy

1

confidence

1

1	36809_at	-2.79788870256583	0	*
2	37311_at	-2.20009414203519	0	*
3	36766_at	-2.15356495523503	0	
4	38894_g_at	-2.11314073543331	0	
5	39179_at	-2.08890598787237	0	
6	38893_at	-2.05723533682216	0	
7	37897_s_at	-2.05026870146261	0	
8	41809_at	1.98458593845403	0	
9	36963_at	-1.95232400595449	0	
10	39301_at	-1.91549367394028	0	

11	40610_at	1.91246286924336	0
12	38879_at	-1.87541355348469	0
13	41338_at	1.86506063801814	0
14	39968_at	-1.81415292791782	0
15	33371_s_at	-1.81111388769192	0
16	37149_s_at	-1.77170759525375	0
17	38895_i_at	-1.77027078711718	0
18	41220_at	1.75387842844952	0
19	37099_at	-1.74839569592051	0
20	40159_r_at	-1.35163593608562	0

AML - BM

samples: 59 / 8

accuracy

1

confidence

0.995997161972555

1	36710_at	-2.29217042550277	0	*
2	32775_r_at	-2.24397275344625	0	*
3	32821_at	-1.98392215005915	0	
4	37149_s_at	-1.94686927462724	0	

5	37015_at	-1.89128914250756	0
6	36894_at	-1.80507021485339	0
7	38735_at	-1.78884482794867	0
8	33752_at	-1.77319451495748	0
9	34654_at	-1.67560279229506	0
10	1115_at	-1.62050106692579	0
11	31859_at	-1.52416410078922	0
12	1980_s_at	1.51765867172316	0
13	36464_at	-1.49540428238676	0
14	38858_at	-1.48511074361835	0
15	38225_at	-1.4790110074487	0
16	39170_at	-1.45392862675606	0
17	39929_at	-1.44420537588163	0
18	36021_at	-1.42322337311917	0
19	32259_at	-1.41395952112425	0
20	41138_at	1.25347154740786	0

AML - CLL

samples: 59 / 8

	<i>accuracy</i>	<i>1</i>		
	<i>confidence</i>	<i>1</i>		
1	36239_at	-3.31028543322741	0	*
2	41220_at	-3.2480863078754	0	
3	1096_g_at	-3.1269759462136	0	
4	36155_at	-3.08191178811872	0	
5	38578_at	-3.06174627261543	0	*
6	34871_at	-3.02230826662657	0	
7	38006_at	-2.88939117591885	0	
8	41165_g_at	-2.87065891259428	0	
9	1105_s_at	-2.81674515012354	0	
10	41166_at	-2.75359060509193	0	
11	31936_s_at	-2.75277577570011	0	
12	33812_at	-2.74332185979714	0	
13	41796_at	-2.71763998725163	0	
14	36894_at	-2.64049311405919	0	
15	38577_at	-2.63072228466709	0	
16	38666_at	-2.61485585331331	0	

17	32597_at	-2.61456952032068	0
18	41847_at	-2.59409998700552	0
19	34830_at	-2.5698161906968	0
20	33266_at	1.336807541194	0

AML - CML

samples: 59 / 10

accuracy

1

confidence

0.956293899622379

1	36464_at	-2.85754269919935	0	*
2	32821_at	-2.55228282645443	0	*
3	31859_at	-2.27761090295808	0	
4	37149_s_at	-2.11494842606363	0	
5	36710_at	-1.94749857224656	0	
6	34546_at	-1.85596431666606	0	
7	33530_at	-1.82614283985583	0	
8	35919_at	-1.74217437339032	0	
9	37099_at	-1.7184463713752	0	
10	36165_at	1.7091639497163	0	

11	37054_at	-1.69705232668157	0
12	31381_at	-1.6873086898061	0
13	37579_at	-1.68217107035442	0
14	33371_s_at	-1.67508882502583	0
15	1117_at	-1.67009743506797	0
16	38894_g_at	-1.66951302748224	0
17	31793_at	-1.63477764661912	0 *
18	40419_at	-1.62639286532631	0
19	37926_at	-1.59510369191926	0
20	40159_r_at	-0.830070056055723	0

BM - CLL

samples: 8 / 8

accuracy

1

confidence

1

1	39070_at	6.29661458968093	0 *
2	37755_at	4.71476584328837	0 *
3	33963_at	4.63206684324173	0
4	38415_at	-4.49254544394577	0

5	36123_at	4.12198883271914	0
6	37615_at	3.82297014835908	0
7	38116_at	3.70165567234484	0
8	38414_at	3.60409203763551	0
9	41220_at	-3.59882846329979	0
10	34871_at	-3.59319336097498	0
11	35643_at	3.56571508955085	0
12	1096_g_at	-3.51858708122275	0
13	33386_at	3.50471765190995	0
14	1884_s_at	3.48564292772594	0
15	37149_s_at	3.4769522926405	0
16	820_at	3.37687376127416	0
17	38269_at	-3.31356010895055	0
18	35995_at	3.26267624054277	0
19	33358_at	3.25001188548107	0
20	33284_at	3.23482135945872	0

BM - CML

samples: 8 / 10

	<i>accuracy</i>	1		
	<i>confidence</i>	1		
1	37625_at	2.87622426554922	0	*
2	41609_at	2.52321020501761	0	*
3	36661_s_at	2.51057654386246	0	
4	1911_s_at	-2.42145340446397	0	
5	854_at	2.37696256335487	0	
6	36773_f_at	2.32488494287137	0	
7	35016_at	2.24094140253387	0	
8	33274_f_at	2.21051775352204	0	
9	38112_g_at	2.13305817504128	0	
10	38194_s_at	2.09822821859324	0	
11	41165_g_at	2.09291822272078	0	
12	33273_f_at	2.0687446585274	0	
13	39179_at	-2.04974106118371	0	
14	432_s_at	2.01424464352775	0	
15	36588_at	1.99886555057795	0	
16	39968_at	-1.98085064661371	0	

17	1385_at	1.98022588084225	0
18	36629_at	-1.9763991250365	0
19	38728_at	1.95859957483225	0
20	38472_at	1.95627106051459	0

CLL - CML

samples: 8 / 10

accuracy

1

confidence

1

1	1105_s_at	6.65345823459692	0	*
2	41609_at	5.09272743129851	0	*
3	1096_g_at	4.79791769602114	0	
4	34210_at	4.5885400157468	0	
5	36155_at	4.51821220572632	0	
6	36766_at	-4.38087516961473	0	
7	41220_at	4.30356291392085	0	
8	41165_g_at	4.29933289075313	0	
9	37625_at	4.27214024229386	0	
10	37027_at	4.17726581707744	0	

11	34871_at	4.11725674890371	0
12	38095_i_at	4.01294758950756	0
13	38578_at	3.96024474623017	0
14	38116_at	-3.93637939332745	0
15	35643_at	-3.90694033464584	0
16	38833_at	3.90073371467641	0
17	41164_at	3.89237729890143	0
18	37344_at	3.8687581898534	0
19	39670_at	3.86448376068684	0
20	35016_at	3.74007150430317	0

2. Analyse: analysis of AML subtypes according to the WHO nomenclature

AMLMLL - samples: 10 / 45

accuracy 1

confidence 0.92125170098711

1	34306_at	1.36682833853864	0	*
2	36881_at	1.25743716610113	0	*

3	38994_at	1.25633105431216	0	*
4	38485_at	1.20820491820515	0	
5	32696_at	1.20289326580336	0	
6	1983_at	-1.20116171703008	0	
7	37026_at	-1.18461413291823	0	
8	138_at	1.18310205413783	0	
9	38812_at	-1.17846157492535	0	
10	33284_at	-1.16681898560395	0	
11	32232_at	1.14845507137154	0	
12	39921_at	1.13232410733091	0	
13	34679_at	-1.12714040987389	0	
14	37992_s_at	1.11986637618528	0	
15	37029_at	1.06646924971963	0	
16	40775_at	-1.06615341562387	0	
17	36709_at	1.04614233632581	0	
18	37809_at	1.03749230715704	0	
19	38097_at	1.03525254247508	0	
20	36608_at	0.747544727295107	0	

AMLMLL - INV16		samples: 10 / 10	
<i>accuracy</i>		1	
<i>confidence</i>		1	
1	38812_at	-3.34686451971904	0 *
2	37407_s_at	-3.22294767554078	0
3	35282_r_at	2.34298696520172	0 *
4	37026_at	-2.25660818336648	0
5	33856_at	2.25212063750729	0
6	32174_at	-2.16867472363265	0
7	33284_at	-2.14901777919516	0
8	38653_at	-2.09296931036988	0
9	1983_at	-2.06674088426528	0
10	32696_at	2.03331671439074	0
11	767_at	-1.99007511677258	0
12	35329_at	1.92663715318122	0
13	36881_at	1.88821561232545	0
14	40767_at	-1.84600140068058	0

15	36095_at	-1.77023425026019	0
16	538_at	-1.75720288873792	0
17	33319_at	1.6982626829354	0
18	38485_at	1.69464482881744	0
19	38747_at	-1.69240449076905	0
20	38994_at	1.50803351291881	0

AMLMLL - OTHER

samples: 10 / 10

accuracy

1

confidence

0.972144217378764

1	36980_at	-1.34035598763443	0	*
2	100_g_at	1.32781895440119	0	*
3	38994_at	1.27848227020726	0	
4	37029_at	1.27656800999718	0	
5	37026_at	-1.24955259337174	0	*
6	37417_at	1.19110502379759	0	*
7	39993_at	-1.18099046398082	0	
8	39118_at	-1.1584453284446	0	

9	36881_at	1.12737149627183	0
10	34251_at	-1.12590878042921	0
11	35813_at	1.10960381779872	0
12	138_at	1.09814796011793	0
13	36945_at	1.09593061163621	0
14	40281_at	1.083400522626	0
15	35941_f_at	1.0833686449051	0
16	36952_at	1.069544205786	0
17	37403_at	-1.06943971961994	0
18	33689_s_at	1.06337639894231	0
19	35372_r_at	-1.05302441823616	0
20	32072_at	1.02664886940357	0

AMLMLL - T1517

samples: 10 / 16

accuracy

1

confidence

1

1	39649_at	3.23957503042803	0	*
2	38435_at	2.60733219271303	0	*

3	38097_at	2.52025252941371	0
4	32229_at	2.40682119042641	0
5	38487_at	-2.31348932548076	0
6	32696_at	2.21878031159682	0
7	38485_at	2.10692284528305	0
8	33284_at	-2.09299435714406	0
9	38824_at	2.08124417022995	0
10	41138_at	-2.03312026813146	0
11	37967_at	1.92254422115649	0
12	33866_at	-1.91543446589406	0
13	32543_at	-1.87715920226866	0
14	1983_at	-1.87444715294745	0
15	35823_at	-1.86189545486519	0
16	36749_at	-1.81025193870165	0
17	38063_at	-1.7878938995328	0
18	39814_s_at	-1.75490742013487	0
19	36843_at	1.74046122003025	0
20	38992_at	1.71753799928796	0

AMLMLL - T821		samples: 10 / 9		
	<i>accuracy</i>	1		
	<i>confidence</i>	1		
1	36881_at	2.29294544811647	0	*
2	32323_at	-1.98347658852059	0	*
3	37811_at	-1.98247325351143	0	
4	38391_at	1.94083259845207	0	
5	33412_at	1.92827460657744	0	
6	33284_at	-1.8385557317965	0	
7	33856_at	1.77909423724864	0	
8	38097_at	1.75444250975416	0	
9	34679_at	-1.72476579402037	0	
10	37399_at	-1.70947276971912	0	
11	36571_at	1.65482279043264	0	
12	35638_at	-1.65089605723885	0	
13	32696_at	1.63638794888669	0	
14	32184_at	1.62897781786406	0	

15	1911_s_at	-1.61083786198679	0
16	34306_at	1.59626133274337	0
17	138_at	1.59241136884495	0
18	41694_at	-1.55909099909815	0
19	32232_at	1.54494819348846	0
20	36608_at	1.1358211663482	0

INV16 -

samples: 10 / 45

accuracy

1

confidence

1

1	37407_s_at	3.02509409963287	0	*
2	767_at	1.85632628490303	0	*
3	245_at	1.70794453836984	0	
4	35282_r_at	-1.55233894025198	0	
5	38465_at	1.52686366669143	0	
6	36095_at	1.40576248502182	0	
7	32174_at	1.39467340729953	0	
8	1385_at	1.35491176363704	0	

9	41609_at	1.33680396130546	0
10	36607_at	1.31728883029627	0
11	34210_at	1.25533053163606	0
12	33731_at	1.18379724417068	0
13	2019_s_at	1.1724338503802	0
14	40456_at	-1.17211851173852	0
15	277_at	1.16888798816433	0
16	931_at	1.16565119574672	0
17	37762_at	1.14260401763247	0
18	35230_at	1.13832458283537	0
19	34780_at	1.12142169279465	0
20	41200_at	1.10294533672324	0

INV16 - OTHER

samples: 10 / 10

accuracy

1

confidence

1

1	37407_s_at	3.18736190788495	0	*
2	37600_at	2.62690062253569	0	*

3	767_at	2.03572561609575	0
4	41609_at	1.96219869102861	0
5	32174_at	1.91764639873215	0
6	41723_s_at	1.8341348306376	0
7	38833_at	1.8197922525705	0
8	38465_at	1.80863491318623	0
9	38095_i_at	1.80209304301982	0
10	1230_g_at	1.64339686952341	0
11	1252_at	1.59751061992943	0
12	32434_at	-1.5885630305188	0
13	40856_at	1.50737403239702	0
14	37762_at	1.49715599199852	0
15	37344_at	1.46932515754743	0
16	35016_at	1.44723563131209	0
17	35078_at	1.44013020473382	0
18	37001_at	1.43580114615375	0
19	33920_at	1.39389220008214	0
20	245_at	1.37591797605968	0

INV16 - T1517

samples: 10 / 16

accuracy

1

confidence

1

1	245_at	4.57658935261639	0	*
2	38833_at	4.25223366871621	0	*
3	38095_i_at	3.57578878481709	0	
4	39649_at	3.23025693895729	0	
5	38096_f_at	3.14225313100266	0	
6	35016_at	3.0787769409051	0	
7	38435_at	3.03350943051849	0	
8	37039_at	2.97439961013438	0	
9	38465_at	2.96526060073085	0	
10	37407_s_at	2.87881711895892	0	
11	34210_at	2.84796613729927	0	
12	41723_s_at	2.82100515486823	0	
13	41471_at	2.80737102015788	0	
14	34789_at	2.75455608102168	0	

15	1052_s_at	2.6975735697327	0
16	36601_at	2.67187833778929	0
17	41096_at	2.59449996104956	0
18	41609_at	2.57402348086536	0
19	37344_at	2.56147220347162	0
20	40698_at	2.54689030859799	0

INV16 - T821

samples: 10 / 9

accuracy

1

confidence

1

1	37407_s_at	3.01984756968935	0	*
2	2019_s_at	2.27319677276044	0	
3	36607_at	2.26121735205867	0	
4	41535_at	2.20248916475367	0	*
5	40198_at	1.86811562002606	0	
6	35264_at	1.84583120098715	0	
7	36661_s_at	1.8131267115673	0	
8	36095_at	1.79878279442616	0	

9	32747_at	1.78653441127702	0
10	40718_at	1.77233756136773	0
11	37326_at	1.76038682206377	0
12	34780_at	1.74785276488982	0
13	39610_at	1.74122046729845	0
14	33390_at	1.73740374189728	0
15	767_at	1.72097134093781	0
16	32080_at	-1.70225469167763	0
17	39358_at	1.695944330956	0
18	37747_at	1.67498682162383	0
19	245_at	1.65171897393137	0
20	33731_at	1.62582771838167	0

OTHER -

samples: 10 / 45

accuracy

0.981818181818182

confidence

0.981818181818182

1	34251_at	1.12590878042921	0	*
2	37018_at	1.10268143578403	0	

3	33920_at	-0.956076703831482 0
4	35941_f_at	-0.90383440767488 0
5	256_s_at	-0.858111816204111 0.01
6	37333_at	0.8275447098375 0
7	32434_at	0.805850409739795 0
8	1959_at	0.796925434525945 0
9	37147_at	-0.773953141034502 0
10	33284_at	-0.771438360960095 0
11	40864_at	-0.770641950715737 0
12	35154_at	-0.764874807980337 0
13	2047_s_at	-0.748787188622726 0
14	41763_g_at	0.748545954599463 0
15	36900_at	-0.74265889729539 0
16	33351_at	0.742532920653334 0
17	36936_at	0.733922207115175 0
18	37263_at	0.729044492680672 0
19	38695_at	-0.71970619250199 0
20	40509_at	0.712799214281053 0

OTHER - T1517

samples: 10 / 16

accuracy

1

confidence

1

1	39649_at	3.30712305398492	0	*
2	40718_at	-2.52673625599382	0	*
3	39775_at	-1.97869028082043	0	
4	34789_at	1.95413968158198	0	
5	32543_at	-1.91464724323262	0	
6	34110_g_at	-1.77793772892734	0	
7	38487_at	-1.76846306892822	0	
8	40493_at	-1.6739728895294	0	
9	40698_at	1.65346991374979	0	
10	41273_at	-1.61494643368443	0	
11	33284_at	-1.59460520214407	0	
12	32434_at	1.57854380538056	0	
13	39755_at	-1.57527382190822	0	
14	40817_at	-1.54437681308404	0	

15	37408_at	-1.53683716438534	0
16	33102_at	1.53530070976794	0
17	1752_at	-1.52886252404363	0
18	37954_at	-1.5109989255419	0
19	38791_at	-1.48386160940786	0
20	34210_at	1.44938674947878	0

OTHER - T821

samples: 10 / 9

accuracy

1

confidence

0.994837795579117

1	32323_at	-1.94417836607133	0	*
2	37811_at	-1.61775423684388	0	*
3	34512_at	-1.39224768490919	0	
4	37809_at	1.31872220085798	0	
5	40585_at	1.31087716877391	0	
6	33284_at	-1.29020750912798	0	
7	38096_f_at	-1.25756828218199	0	
8	36973_at	1.23300907353238	0	

9	35940_at	-1.20559489876876	0
10	38808_at	-1.18153953430958	0
11	37333_at	1.17979557242332	0
12	2047_s_at	-1.17934561734238	0
13	AFFX-HUMRGE/M10098_M_at	-1.15756874447998	0
14	958_s_at	1.1376378956	0
15	34251_at	1.12590878042921	0
16	38963_i_at	-1.12200244261352	0
17	35638_at	-1.12014975713644	0
18	38095_i_at	-1.10572791785236	0
19	37657_at	-1.08109523793911	0
20	40718_at	0.918288266614732	0

T1517 - samples: 16 / 39

accuracy 1

confidence 0.99537936517205

1	39649_at	-3.29831494694965	0	*
2	40718_at	2.08511115510612	0	*

3	38487_at	2.00096141225403	0	*
4	34110_g_at	1.76946763277471	0	
5	34789_at	-1.70643590139573	0	
6	38435_at	-1.66171359352607	0	
7	32543_at	1.59263172662039	0	
8	41273_at	1.54397178886438	0	
9	40493_at	1.48615605789895	0	
10	38096_f_at	-1.44819099507958	0	
11	41471_at	-1.41828217671556	0	
12	37954_at	1.41406051783378	0	
13	33454_at	1.39832642238269	0	
14	38791_at	1.38083401177366	0	
15	41096_at	-1.36447605743032	0	
16	1752_at	1.36363148385769	0	
17	38833_at	-1.34891815086687	0	
18	210_at	-1.34320613976446	0	
19	35016_at	-1.33685666840696	0	
20	37669_s_at	0.806171390298286	0	

T1517 - T821		samples: 16 / 9	
	<i>accuracy</i>	1	
	<i>confidence</i>	1	
1	40718_at	3.23930438679201 0	*
2	39649_at	-3.19787649222746 0	*
3	40698_at	-3.08468795621776 0	
4	38096_f_at	-2.65789275034265 0	
5	39775_at	2.36672318019601 0	
6	38487_at	2.29609697942891 0	
7	33121_g_at	-2.21859945215003 0	
8	35016_at	-1.96619441751917 0	
9	38095_i_at	-1.91141006266887 0	
10	32506_at	-1.88419268611225 0	
11	38833_at	-1.85079137548356 0	
12	34110_g_at	1.85075648886345 0	
13	41096_at	-1.8279606340398 0	
14	38391_at	1.81966548635468 0	

15	35766_at	1.75448820173577	0
16	34789_at	-1.71046499814806	0
17	41609_at	-1.710217028597	0
18	41273_at	1.70663861548637	0
19	37344_at	-1.69281730857466	0
20	35340_at	1.69006593600413	0

T821 -

samples: 9 / 46

accuracy

1

confidence

0.920027437519393

1	37811_at	1.59605072597366	0	*
2	38391_at	-1.3878317468135	0	
3	35638_at	1.38266687057184	0	*
4	32323_at	1.35561326937612	0	
5	35940_at	1.20094762805468	0	*
6	36973_at	-1.17706120019907	0	
7	35264_at	-1.10943417036523	0	
8	361_at	1.07264489085601	0	

9	36802_at	-1.02457173409803	0
10	34512_at	1.0204248889286	0
11	35939_s_at	0.955125481450532	0
12	39061_at	-0.947115729172708	0
13	37326_at	-0.935233446940231	0
14	32747_at	-0.930843404980031	0
15	1096_g_at	0.927398573506987	0
16	33121_g_at	0.923255276498333	0 *
17	41535_at	-0.916652918883009	0
18	37023_at	-0.915934376270622	0
19	38780_at	-0.915816135921152	0

3. Analyse: analysis of ALL subtypes

ALL814 -		samples: 3 / 14	
accuracy		1	
confidence		1	
1	1402_at	2.08175003568258	0.01 *
2	37747_at	2.03525291878921	0 *

3	37701_at	1.72252048284758	0.01
4	2042_s_at	-1.63373519277864	0
5	35260_at	-1.63074548017429	0
6	1476_s_at	-1.58695680100552	0
7	32616_at	1.57366205688451	0
8	932_i_at	-1.57233356229385	0
9	36139_at	-1.5665197341194	0
10	39730_at	-1.5464188647031	0.01
11	2024_s_at	1.48918618192137	0.01
12	38730_at	-1.45475301578891	0.01
13	37021_at	1.45440716568168	0
14	933_f_at	-1.42175300666003	0
15	41396_at	-1.38553827410353	0
16	33856_at	1.37781449850137	0
17	33905_at	1.3359321134002	0.01

ALL814 - ALLMLL

samples: 3 / 4

accuracy

1

	<i>confidence</i>	1	
1	2042_s_at	-8.02342094912714 0.05	*
2	36638_at	-4.58127332202829 0.02	
3	1474_s_at	-4.09073883260025 0.03	*
4	706_at	-3.85465872728703 0.02	
5	38994_at	-3.74888987537358 0.02	
6	34785_at	-3.3713121522884 0.03	
7	36798_g_at	-3.35179120581516 0	
8	41191_at	-3.25108066126486 0.01	
9	39827_at	-3.14944671750591 0.02	
10	585_at	-3.09495658747361 0.04	
11	2069_s_at	-3.01980201927276 0.02	
12	529_at	2.93352551602605 0.01	
13	307_at	2.92372091093276 0.03	
14	32842_at	-2.85788132874268 0.01	
15	36873_at	-2.84199424616029 0.05	
16	41747_s_at	-2.76420890085279 0.01	

ALL814 - ALLPH		samples: 3 / 7	
<i>accuracy</i>		1	
<i>confidence</i>		1	
1	35260_at	-2.82900147590099	0.01 *
2	41177_at	2.74938757132087	0 *
3	36638_at	-2.41641563333395	0.01
4	38767_at	-2.40416010568405	0.01
5	37747_at	2.39180707441687	0
6	39327_at	-2.27856651600595	0
7	1476_s_at	-2.09613072968554	0.02
8	1636_g_at	-2.00644064085741	0.01
9	37159_at	-1.98769010758559	0
10	932_i_at	-1.95869341917388	0
11	38994_at	-1.94783634512686	0.02
12	1402_at	1.91294884399227	0
13	32319_at	-1.89265256004687	0.01
14	2047_s_at	-1.89118154910995	0
15	40936_at	-1.84560154590494	0

16	39730_at	-1.84157870686046	0.03
17	39089_at	-1.83344549691856	0
18	41734_at	-1.82721322918029	0.01
19	39755_at	-1.80690655801942	0.03

ALL814 - ALLT

samples: 3 / 3

accuracy

1

confidence

1

1	36103_at	3.43807291883285	0.01	*
2	35350_at	3.3144051465682	0.04	
3	41654_at	-3.10101195313041	0.04	*

ALLMLL -

samples: 4 / 13

accuracy

1

confidence

1

1	36873_at	2.83046978285357	0	*
2	36638_at	2.81082924166381	0	*
3	33358_at	2.41284542345819	0	

4	34785_at	2.01800062696643	0
5	36667_at	2.00264026114972	0
6	41503_at	1.98278140811591	0
7	36690_at	1.97928285044649	0.01
8	706_at	1.96737076450007	0
9	32842_at	1.88883935305863	0
10	41747_s_at	1.87619134543011	0
11	32145_at	1.87136682311337	0
12	36798_g_at	1.76515008934463	0.01
13	41191_at	1.7369773616741	0
14	40763_at	1.69441997605083	0
15	585_at	1.66246850330104	0
16	41470_at	1.53671027688439	0
17	40786_at	1.52293758990032	0
18	38037_at	1.50762328192198	0.01
19	34583_at	1.46227478562542	0
20	1140_at	1.46133065433595	0

ALLMLL - ALLPH		samples: 4 / 7		
	<i>accuracy</i>	1		
	<i>confidence</i>	1		
1	40723_at	3.55841873411154	0	*
2	706_at	3.32668949661753	0	*
3	41191_at	2.96542484991746	0	
4	36638_at	2.84067512400178	0	
5	36873_at	2.8258041781711	0	
6	36690_at	2.54358082956883	0	
7	33358_at	2.34079500414888	0	
8	36798_g_at	2.21311555975342	0.01	
9	36667_at	2.20932580996057	0.01	
10	41177_at	2.1413450003396	0	
11	40865_at	2.11221046250059	0	
12	37967_at	-2.08412772392346	0	
13	34892_at	-2.08369333371306	0	
14	40396_at	1.96552338894503	0	
15	1140_at	1.96261636340905	0	

16	33134_at	-1.95145751139773	0
17	32842_at	1.84503319654406	0
18	41503_at	1.8284794750916	0
19	32145_at	1.82248695271075	0
20	40763_at	1.78804175908387	0.01

ALLMLL - ALLT

samples: 4 / 3

accuracy

1

confidence

1

1	2069_s_at	13.292701923441	0	*
2	41153_f_at	10.2582391724747	0	*
3	41156_g_at	5.75960819662385	0.01	
4	33352_at	4.58870845894255	0	
5	36638_at	4.58127332202829	0.03	
6	1185_at	4.45457229345442	0.01	
7	37775_at	-4.11123301947466	0.02	
8	1105_s_at	-4.04867441577307	0.03	
9	41155_at	3.98831214950398	0.01	

10	38994_at	3.88924207710779	0.02
11	34785_at	3.83690018368942	0.01
12	32819_at	3.567056723698	0.03
13	38319_at	-3.55471475398643	0.01
14	2045_s_at	3.54943843148795	0.02
15	40159_r_at	3.40746200289675	0.03
16	39136_at	-3.36701895470486	0.02
17	1110_at	-3.33969464270628	0.01
18	38017_at	3.32515685260135	0.01
19	605_at	-3.28310118648462	0.02

4. Analyse: other analyses

ALLPH - samples: 7 / 10

accuracy 1

confidence 1

1	1389_at	1.58617196971584	0	*
2	41734_at	1.55949651759221	0	*
3	38336_at	1.52692526781459	0	

4	33134_at	1.449713769608	0
5	36878_f_at	1.36077477960263	0
6	39755_at	1.27483851783738	0
7	38833_at	1.2244093710462	0
8	33924_at	1.22263315100349	0
9	34362_at	1.1962046547055	0
10	36536_at	1.19336569573264	0
11	37344_at	1.18918159634593	0
12	38095_i_at	1.16331309702494	0
13	35260_at	1.12932649576543	0
14	41177_at	-1.07976913600882	0
15	38096_f_at	1.05014739949744	0.01
16	36773_f_at	1.0492226005037	0
17	39824_at	1.03626825828771	0
18	31898_at	1.02765158070601	0
19	1636_g_at	1.0227576964995	0
20	41609_at	0.997013086295946	0

ALLPH - ALLT

samples: 7 / 3

	<i>accuracy</i>	1		
	<i>confidence</i>	1		
1	1105_s_at	-4.05162267253209	0	*
2	38319_at	-3.66580320533053	0.03	*
3	38096_f_at	2.88234070062166	0.02	
4	37039_at	2.80755189593111	0	
5	35016_at	2.77774834690928	0.01	
6	38833_at	2.75560710134977	0.01	
7	39262_at	-2.59234132448068	0	
8	32649_at	-2.55542908459441	0	
9	33821_at	-2.5421725262322	0.01	
10	41609_at	2.5109183575568	0	
11	38147_at	-2.50135496035854	0	
12	38095_i_at	2.48939716688646	0.02	
13	37739_at	-2.44732228148107	0	
14	38894_g_at	2.42422840620003	0.01	
15	36638_at	2.41641563333395	0	

16	38361_g_at	2.38116082851993	0.01
17	2059_s_at	-2.37547551809124	0.01
18	33425_at	-2.36441631934975	0
19	38949_at	-2.27455845085004	0
20	39755_at	2.26518913381284	0

ALLT -

samples: 3 / 14

accuracy

1

confidence

1

1	38319_at	3.50494628126444	0	*
2	33821_at	2.86458211053638	0	*
3	1105_s_at	2.7919896009269	0	
4	38147_at	2.2999876938771	0	
5	38949_at	2.275851563485	0	
6	33425_at	2.24691287113975	0	
7	40407_at	2.23626457040595	0	
8	1110_at	2.23213485898084	0	
9	39136_at	2.21536950680885	0	

10	41535_at	2.20104335983474	0
11	2059_s_at	2.17544015063967	0
12	39262_at	2.14503507257872	0
13	34367_at	2.14251924457163	0
14	35016_at	-2.12822205034103	0
15	38096_f_at	-2.0151362322022	0
16	37775_at	2.0098435918241	0.01
17	38917_at	2.00844440766432	0
18	33238_at	2.00529430466423	0
19	1498_at	1.98727437856937	0
20	41163_at	1.90540704553591	0

ALLPHNEG - ALLPHPOS

samples: 11 / 7

accuracy

1

confidence

0.946908445764721

1	38336_at	-1.5382379030083	0	*
2	33134_at	-1.30650437502273	0	*
3	39755_at	-1.28612797222091	0	

4	1636_g_at	-1.04852861613762 0
5	38833_at	-1.04767357167583 0
6	41177_at	1.04154428480732 0
7	34168_at	-1.00022056220148 0
8	38096_f_at	-0.991139993364388 0
9	38095_i_at	-0.969632957696579 0
10	33924_at	-0.965257886268051 0
11	39756_g_at	-0.964856826724863 0
12	38312_at	-0.964240310753493 0
13	36878_f_at	-0.961827994429321 0
14	41193_at	-0.957818027300299 0
15	37384_at	-0.934644823332001 0
16	32706_at	0.916645445316056 0
17	33441_at	-0.910220742840358 0
18	41547_at	0.895837845645142 0
19	36773_f_at	-0.884139970624711 0
20	32649_at	0.833759113455451 0

Table 21

Affy met rix_ ID	Description_microarray	Symbo l	Description_Net Affx	Chrom osome
100 _g_ _at	Y08200 /FEATURE= /DEFINITION=HSRABGTRA Homo sapiens mRNA for rab geranylgeranyl transferase, alpha-subunit	RABG GTA	Rab geranylgeranyltr ansferase, alpha subunit	14q11. 2
105 2_s _at	M83667 /FEATURE=mRNA /DEFINITION=HUMNFIL6BA Human NF-IL6-beta protein mRNA, complete cds	CEBP D	CCAAT/enhanc er binding protein (C/EBP), delta	8p11.2 -p11.1
106 2_g _at	U00672 /FEATURE= /DEFINITION=U00672 Human interleukin-10 receptor mRNA, complete cds	IL10R A	interleukin 10 receptor, alpha	11q23
109 6_g _at	M28170 /FEATURE= /DEFINITION=HUMCSPC Human cell surface protein CD19 (CD19) gene, complete cds	CD19	CD19 antigen	16p11. 2
110 5_s _at	M12886 /FEATURE= /DEFINITION=HUMTCBY Human T- cell receptor active beta-chain mRNA, complete cds	TRB	T cell receptor beta locus	7q35
111 0_a	M21624 /FEATURE=mRNA /DEFINITION=HUMTCRGC Human T-	TRD	T cell receptor delta locus	14q11. 2

t	cell receptor delta chain mRNA (VJC-region), complete cds		delta locus	2
111 5_a t	M25897 /FEATURE=mRNA /DEFINITION=HUMPF4A Human platelet factor 4 (PF4) mRNA, complete cds	PF4	platelet factor 4	4q12- q21
111 7_a t	L27943 /FEATURE=mRNA /DEFINITION=HUMCYDE Homo sapiens cytidine deaminase (CDA) mRNA, complete cds	CDA	cytidine deaminase	1p36.2 -p35
114 0_a t	L25851 /FEATURE= /DEFINITION=HUMINAE Homo sapiens integrin alpha E precursor, mRNA, complete cds	ITGAE	"integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)"	17p13
118 5_a t	D49410 /FEATURE=expanded_cds /DEFINITION=HUMIL3RA12 Human gene for interleukin 3 receptor alpha subunit, exon 12 and partial cds			
121 7_g _at	X07109 /FEATURE=cds /DEFINITION=HSPKCB2A Human mRNA for protein kinase C (PKC) type beta II	PRKC B1	protein kinase C, beta 1	16p11. 2
123 0_g _at	U78556 /FEATURE= /DEFINITION=HSU78556 Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete	CRA	cisplatin resistance associated	1q12- q21

	cds			
125 2_a t	M73547 /FEATURE= /DEFINITION=HUMPOLLA Human polyposis locus (DP1 gene) mRNA, complete cds	D5S34 6	DNA segment, single copy probe LNS- CAI/LNS-CAII (deleted in polyposis	5q22- q23
137 _at	U65404 /FEATURE= /DEFINITION=HSU65404 Human erythroid-specific transcription factor EKLF mRNA, complete cds	KLF1	Kruppel-like factor 1 (erythroid)	19p13. 13- p13.12
138 5_a t	M77349 /FEATURE= /DEFINITION=HUMTGFBIG Human transforming growth factor-beta induced gene product (BIGH3) mRNA, complete cds	TGFB1	transforming growth factor, beta-induced, 68kD	5q31
138 9_a t	J03779 /FEATURE=mRNA /DEFINITION=HUMCALLA Human common acute lymphoblastic leukemia antigen (CALLA) mRNA, complete cds	MME	membrane metallo- endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	3q25.1 -q25.2
138 _at	U66464 /FEATURE= /DEFINITION=HSU66464 Human hematopoietic progenitor kinase (HPK1) mRNA, complete cds	MAP4 K1	mitogen- activated protein kinase kinase kinase kinase 1	19q13. 1- q13.4
140 2_a t	M16038 /FEATURE= /DEFINITION=HUMLYN Human lyn mRNA encoding a tyrosine kinase	LYN	v-yes-1 Yamaguchi sarcoma viral	8q13

t	mRNA encoding a tyrosine kinase		related oncogene homolog	
147 4_s _at	U22376 /FEATURE=cds#3 /DEFINITION=HSU22376 Human (c- myb) gene, complete primary cds, and five complete alternatively spliced cds			
147 6_s _at	U22376 /FEATURE=cds#5 /DEFINITION=HSU22376 Human (c- myb) gene, complete primary cds, and five complete alternatively spliced cds			
149 5_a t	M34057 /FEATURE= /DEFINITION=HUMTGFB1B Human transforming growth factor-beta 1 binding protein mRNA, complete cds	LTBP1	latent transforming growth factor beta binding protein 1	2p22- p21
149 7_a t	L04270 /FEATURE= /DEFINITION=HUMTNFRRP Homo sapiens (clone CD18) tumor necrosis factor receptor 2 related protein mRNA, complete cds	LTBR	lymphotoxin beta receptor (TNFR superfamily, member 3)	12p13
149 8_a t	L05148 /FEATURE= /DEFINITION=HUMTYRKIN Human protein tyrosine kinase related mRNA sequence			
152 9_a t	U50534 /FEATURE= /DEFINITION=HSU50534 Human BRCA2 region, mRNA sequence CG003			

163 6_g _at	U07563 /FEATURE=Poly_A_Site#1 /DEFINITION=HSABLGR3 Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds			
175 2_a t	AD000092 /FEATURE=cds#6 /DEFINITION=CH19HHR23 Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence			
188 4_s _at	M15796 /FEATURE= /DEFINITION=HUMCYL Human cyclin protein gene, complete cds	PCNA	proliferating cell nuclear antigen	20pter- p12
191 1_s _at	M60974 /FEATURE= /DEFINITION=HUMGADD45 Human growth arrest and DNA-damage- inducible protein (gadd45) mRNA, complete cds	GADD 45A	growth arrest and DNA- damage- inducible, alpha	1p31.2 -p31.1
195 9_a t	D88674 /FEATURE= /DEFINITION=D88674 Homo sapiens mRNA for antizyme inhibitor, complete cds	OAZIN	ornithine decarboxylase antizyme inhibitor	8q22.3
198 0_s _at	X58965 /FEATURE= /DEFINITION=HSNM23H2G H.sapiens RNA for nm23-H2 gene	NME2	non-metastatic cells 2, protein (NM23B) expressed in	17q21. 3
198 3_a	X68452 /FEATURE=cds /DEFINITION=HSCYCD2 H.sapiens	CCND 2	cyclin D2	12p13

t	mRNA for cyclin D2	2		
201 9_s _at	M68892 /FEATURE= /DEFINITION=HUMINTB7 Human integrin beta-7 subunit mRNA, complete cds	ITGB7	integrin, beta 7	12q13. 13
202 4_s _at	M79321 /FEATURE= /DEFINITION=HUMLYNTK Human Lyn B protein mRNA, complete cds	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	8q13
204 2_s _at	M15024 /FEATURE= /DEFINITION=HUMCMYBLA Human c-myb mRNA, complete cds	MYB	v-myb avian myeloblastosis viral oncogene homolog	6q22- q23
204 5_s _at	M16592 /FEATURE=mRNA /DEFINITION=HUMHCKB Human hemopoietic cell protein-tyrosine kinase (HCK) gene, complete cds, clone HK24	HCK	hemopoietic cell kinase	20q11- q12
204 7_s _at	M23410 /FEATURE= /DEFINITION=HUMPLAKO Human plakoglobin (PLAK) mRNA, complete cds	JUP	junction plakoglobin	17q21
205 9_s _at	M36881 /FEATURE=mRNA /DEFINITION=HUMLCKAA Human lymphocyte-specific protein tyrosine kinase (lck) mRNA, complete cds	LCK	lymphocyte- specific protein tyrosine kinase	1p35- p34.3

206 9_s _at	L23805 /FEATURE= /DEFINITION=HUMCATENIN Human alpha1(E)-catenin mRNA, complete cds	CTNN A1	catenin (cadherin- associated protein), alpha 1 (102kD)	5q31
210 _at	M95678 /FEATURE= /DEFINITION=HUMPLCB2A Homo sapiens phospholipase C-beta-2 mRNA, complete cds	PLCB2	phospholipase C, beta 2	15q15
245 _at	M25280 /FEATURE= /DEFINITION=HUMLNHR Human lymph node homing receptor mRNA, complete cds	SELL	selectin L (lymphocyte adhesion molecule 1)	1q23- q25
256 _s_ _at	M14199 /FEATURE= /DEFINITION=HUMLAMR Human laminin receptor (2H5 epitope) mRNA, 5 end	LAMR 1	laminin receptor 1 (67kD, ribosomal protein SA)	3p21.3
277 _at	L08246 /FEATURE= /DEFINITION=HUMMCL1X Human myeloid cell differentiation protein (MCL1) mRNA			
307 _at	J03600 /FEATURE= /DEFINITION=HUMLOX5 Human lipoxygenase mRNA, complete cds	ALOX5	arachidonate 5- lipoxygenase	10q11. 2
313 81_ _at	Cluster Incl. AF076483:Homo sapiens peptidoglycan recognition protein precursor (PGRP) mRNA, complete cds /cds=(44,634) /gb=AF076483 /gi=3342532 /ug=Hs.137583 /len=690	PGLY RP	peptidoglycan recognition protein	19q13. 2- q13.3

317 93_ at	Cluster Incl. AL036554:DKFZp564J2262_r1 Homo sapiens cDNA, 5 end /clone=DKFZp564J2262 /clone_end=5 /gb=AL036554 /gi=5927801 /ug=Hs.1379 /len=517	DEFA3	defensin, alpha 3, neutrophil-specific	8pter-p23.3
318 59_ at	Cluster Incl. J05070:Human type IV collagenase mRNA, complete cds /cds=(19,2142) /gb=J05070 /gi=177204 /ug=Hs.151738 /len=2334	MMP9	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)	20q11.2-q13.1
318 70_ at	Cluster Incl. X14046:Human mRNA for leukocyte antigen CD37 /cds=(63,908) /gb=X14046 /gi=29793 /ug=Hs.153053 /len=1125	CD37	CD37 antigen	19p13-q13.4
318 98_ at	Cluster Incl. D86967:Human mRNA for KIAA0212 gene, complete cds /cds=(58,2031) /gb=D86967 /gi=1504007 /ug=Hs.154332 /len=6072	KIAA0212	KIAA0212 gene product	3p25.3
319 36_ s_at	Cluster Incl. AB007890:Homo sapiens KIAA0430 mRNA, complete cds /cds=(0,3172) /gb=AB007890 /gi=2887438 /ug=Hs.166163 /len=6011	KIAA0430	KIAA0430 gene product	16p13.12
320 72_ at	Cluster Incl. U40434:Human mesothelin or CAK1 antigen precursor mRNA, complete cds /cds=(99,1985) /gb=U40434 /gi=1145723 /ug=Hs.155981 /len=2114	MSLN	mesothelin	16p13.3

320 80_ at	Cluster Incl. L11669:Human tetracycline transporter-like protein mRNA, complete cds /cds=(120,1487) /gb=L11669 /gi=307501 /ug=Hs.157145 /len=1758	TETR AN	tetracycline transporter-like protein	4p16.3
321 45_ at	Cluster Incl. X58141:Human mRNA for erythrocyte adducin alpha subunit /cds=(154,2367) /gb=X58141 /gi=28381 /ug=Hs.183706 /len=3905			
321 66_ at	Cluster Incl. AB028950:Homo sapiens mRNA for KIAA1027 protein, partial cds /cds=(0,5088) /gb=AB028950 /gi=5689390 /ug=Hs.18420 /len=5542	TLN1	talin 1	9p13
321 74_ at	Cluster Incl. AF015926:Homo sapiens ezrin-radixin-moesin binding phosphoprotein-50 mRNA, complete cds /cds=(212,1288) /gb=AF015926 /gi=3220018 /ug=Hs.184276 /len=1984	SLC9A 3R1	solute carrier family 9 (sodium/hydrog en exchanger), isoform 3 regulatory factor 1	17q25. 2
321 84_ at	Cluster Incl. X61118:Human TTG-2 mRNA for a cysteine rich protein with LIM motif /cds=UNKNOWN /gb=X61118 /gi=663012 /ug=Hs.184585 /len=2292	LMO2	LIM domain only 2 (rhombotin- like 1)	11p13
322 29_ at	Cluster Incl. AF038957:Homo sapiens translation initiation factor 4e mRNA, complete cds /cds=(58,768) /gb=AF038957 /gi=3329383 /ug=Hs.19122 /len=961	EIF4E L3	eukaryotic translation initiation factor 4E-like 3	2q37.1

322 32_ at	Cluster Incl. AF047181:Homo sapiens NADH-ubiquinone oxidoreductase subunit CI-SGDH mRNA, complete cds /cds=(6,575) /gb=AF047181 /gi=2909853 /ug=Hs.19236 /len=1034	NDUF B5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGD)	3q27.1
322 59_ at	Cluster Incl. AB002386:Human mRNA for KIAA0388 gene, complete cds /cds=(100,2343) /gb=AB002386 /gi=2224716 /ug=Hs.194669 /len=4606	EZH1	enhancer of zeste (Drosophila) homolog 1	17q21. 1- q21.3
323 19_ at	Cluster Incl. AL022310:dJ395P12.2 (tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L)) /cds=(137,688) /gb=AL022310 /gi=3646083 /ug=Hs.181097 /len=3470			
323 23_ at	Cluster Incl. M63582:Human preprothyrotropin-releasing hormone gene /cds=(8,736) /gb=M63582 /gi=190297 /ug=Hs.182231 /len=1457			
324 34_ at	Cluster Incl. D10522:Homo sapiens mRNA for 80K-L protein, complete cds /cds=(369,1367) /gb=D10522 /gi=219893 /ug=Hs.75607 /len=2589	MACS	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K- L)	6q22.2
325 06_ at	Cluster Incl. AB029031:Homo sapiens mRNA for KIAA1108 protein, partial cds /cds=(0,2291) /gb=AB029031 /gi=5689552 /ug=Hs.69472 /len=2576	TBC1 D1	TBC1 (tre- 2/USP6, BUB2, cdc16) domain family, member 1	4

			1	
325 30_ at	Cluster Incl. X56468:Human mRNA for 14.3.3 protein, a protein kinase regulator /cds=(125,862) /gb=X56468 /gi=23221 /ug=Hs.74405 /len=1862	YWHA Q	tyrosine 3-monooxygenase /tryptophan 5-monooxygenase activation protein, theta polypeptide	22q12-qter
325 43_ at	Cluster Incl. M84739:Human autoantigen calreticulin mRNA, complete cds /cds=(108,1361) /gb=M84739 /gi=179881 /ug=Hs.75525 /len=1937	CALR	calreticulin	19p13.3-p13.2
325 97_ at	Cluster Incl. X76061:H.sapiens p130 mRNA for 130K protein /cds=(69,3488) /gb=X76061 /gi=416030 /ug=Hs.79362 /len=4835	RBL2	retinoblastoma-like 2 (p130)	16q12.2
326 16_ at	Cluster Incl. M16038:Human lyn mRNA encoding a tyrosine kinase /cds=(297,1835) /gb=M16038 /gi=187268 /ug=Hs.80887 /len=2298	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	8q13
326 49_ at	Cluster Incl. X59871:Human TCF-1 mRNA for T cell factor 1 (splice form C) /cds=(79,885) /gb=X59871 /gi=36789 /ug=Hs.169294 /len=2910	TCF7	transcription factor 7 (T-cell specific, HMG-box)	5q31.1
326 96_ at	Cluster Incl. X59841:Human PBX3 mRNA /cds=UNKNOWN /gb=X59841 /gi=35314 /ug=Hs.171680 /len=2581	PBX3	pre-B-cell leukemia transcription	9q33-q34

at	/gi=35314 /ug=Hs.171680 /len=2581		factor 3	
327 06_ at	Cluster Incl. X89887:Homo sapiens mRNA for WD repeat protein (HIRA) /cds=(220,3273) /gb=X89887 /gi=3928218 /ug=Hs.172350 /len=4018	HIRA	HIR (histone cell cycle regulation defective) homolog A (S. cerevisiae)	22q11.21
327 47_ at	Cluster Incl. X05409:Human RNA for mitochondrial aldehyde dehydrogenase I ALDH I (EC 1.2.1.3) /cds=(36,1586) /gb=X05409 /gi=28605 /ug=Hs.195432 /len=1989	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	12q24.2
327 75_ r_at	Cluster Incl. AB006746:Homo sapiens hMmTRA1b mRNA, complete cds /cds=(256,1212) /gb=AB006746 /gi=3510296 /ug=Hs.198282 /len=2077	PLSC R1	phospholipid scramblase 1	3q23
328 00_ at	Cluster Incl. U66306:Human retinoid X receptor alpha mRNA, 3 UTR, partial sequence /cds=UNKNOWN /gb=U66306 /gi=3411007 /ug=Hs.20084 /len=3772			
328 19_ at	Cluster Incl. AJ223352:Homo sapiens mRNA for histone H2B, clone pjG4-5-14 /cds=(16,396) /gb=AJ223352 /gi=3255996 /ug=Hs.20418 /len=793	H2BFA	H2B histone family, member A	6p21.3
328 21_ at	Cluster Incl. AI762213:wi54d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394055 /clone_end=3 /gb=AI762213 /gi=5177880 /ug=Hs.204238 /len=677	LCN2	lipocalin 2 (oncogene 24p3)	9q34

328 42_ at	Cluster Incl. X89984:H.sapiens mRNA for BCL7A protein /cds=(953,1648) /gb=X89984 /gi=929614 /ug=Hs.211563 /len=4522	BCL7A	B-cell CLL/lymphoma 7A	12q24.13
331 02_ at	Cluster Incl. D67031:Homo sapiens ADDL mRNA for adducin-like protein, complete cds /cds=(183,2207) /gb=D67031 /gi=2696053 /ug=Hs.8110 /len=2920	ADD3	adducin (gamma) 3	10q24.2-q24.3
331 21_ g_a t	Cluster Incl. AF045229:Homo sapiens regulator of G protein signaling 10 mRNA, complete cds /cds=(132,635) /gb=AF045229 /gi=2906029 /ug=Hs.82280 /len=753	RGS10	regulator of G-protein signalling 10	10q25
331 34_ at	Cluster Incl. AB011083:Homo sapiens mRNA for KIAA0511 protein, partial cds /cds=(0,2802) /gb=AB011083 /gi=3043545 /ug=Hs.8402 /len=3563	ADCY3	adenylate cyclase 3	2p24-p22
332 38_ at	Cluster Incl. U23852:Human T-lymphocyte specific protein tyrosine kinase p56lck (lck) abberant mRNA, complete cds /cds=(59,1150) /gb=U23852 /gi=775207 /ug=Hs.1765 /len=2129			
332 66_ at	Cluster Incl. AF015254:Homo sapiens serine/threonine kinase (STK-1) mRNA, complete cds /cds=(58,1101) /gb=AF015254 /gi=4090840 /ug=Hs.180655 /len=1234	STK12	serine/threonine kinase 12	17p13.1

332 73_ f_at	Cluster Incl. X57809:Human rearranged immunoglobulin lambda light chain mRNA /cds=(114,815) /gb=X57809 /gi=33714 /ug=Hs.181125 /len=915	IGL	immunoglobulin lambda locus	22q11. 1- q11.2
332 74_ f_at	Cluster Incl. M18645:Human Ig rearranged lambda-chain mRNA VJC- region subgroup lambda-IV from heterohybridoma H6-3C4 /cds=(30,731) /gb=M18645 /gi=186103 /ug=Hs.181125 /len=872	IGL	immunoglobulin lambda locus	22q11. 1- q11.2
332 84_ at	Cluster Incl. M19507:Human myeloperoxidase mRNA, complete cds /cds=UNKNOWN /gb=M19507 /gi=188657 /ug=Hs.1817 /len=3215	MPO	myeloperoxidas e	17q23. 1
333 19_ at	Cluster Incl. AF009674:Homo sapiens axin (AXIN) mRNA, partial cds /cds=(0,2703) /gb=AF009674 /gi=2252819 /ug=Hs.184434 /len=3385	AXIN1	axin	16p13. 3
333 51_ at	Cluster Incl. AF064607:Homo sapiens GC20 protein mRNA, complete cds /cds=(70,411) /gb=AF064607 /gi=3152667 /ug=Hs.21756 /len=812	GC20	translation factor sui1 homolog	3p21.3 3
333 52_ at	Cluster Incl. X57985:H.sapiens genes for histones H2B.1 and H2A /cds=(42,422) /gb=X57985 /gi=510989 /ug=Hs.2178 /len=2223			
333 58_ at	Cluster Incl. W29087:56b8 Homo sapiens cDNA /gb=W29087 /gi=1309053 /ug=Hs.21894 /len=877	KIAA1 157	KIAA1157 protein	12q13. 3- q14.1

at	/gi=1309053 /ug=Hs.21894 /len=877			q14.1
333 71_ s_at	Cluster Incl. U59877:Human low-Mr GTP-binding protein (RAB31) mRNA, complete cds /cds=(60,644) /gb=U59877 /gi=1388194 /ug=Hs.223025 /len=907	RAB31	RAB31, member RAS oncogene family	18p11.3
333 86_ at	Cluster Incl. Z97630:Human DNA sequence from clone 466N1 on chromosome 22q12-13 Contains H1F0(H1 histone family, member 0) gene, 2-amino-3-ketobutyrate -CoA ligase(nuclear gene encoding mitochondrial protein), GALR3 (galanin receptor) gene, ESTs, GSSs an			
333 90_ at	Cluster Incl. AA203487:zx53d03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446213 /clone_end=5 /gb=AA203487 /gi=1799460 /ug=Hs.226237 /len=863		ESTs	
334 12_ at	Cluster Incl. AI535946:vicpro2.D07.r Homo sapiens cDNA, 5 end /clone_end=5 /gb=AI535946 /gi=4450081 /ug=Hs.227751 /len=647	LGALS 1	lectin, galactoside-binding, soluble, 1 (galectin 1)	22q13.1
334 14_ at	Cluster Incl. X57398:Human mRNA for pM5 protein /cds=(0,3572) /gb=X57398 /gi=35526 /ug=Hs.227823 /len=4086	PM5	pM5 protein	16p13.11
334 25_ at	Cluster Incl. X97548:H.sapiens mRNA for TIF1beta zinc finger protein /cds=(361,2868) /gb=X97548 /gi=1524108 /ug=Hs.228059 /len=3035	TRIM2 8	tripartite motif-containing 28	5

	/gi=1524108 /ug=Hs.228059 /len=3035			
334 41_ at	"Cluster Incl. L41143:Homo sapiens expressed pseudo TCTA mRNA at t(1;3) translocation site, complete cds /cds=(221,532) /gb=L41143 /gi=736684 /ug=Hs.232069 /len=2146"			
334 54_ at	Cluster Incl. AF016903:Homo sapiens agrin precursor mRNA, partial cds /cds=(0,6080) /gb=AF016903 /gi=2988421 /ug=Hs.234137 /len=7032	AGRN	agrin	1p36.3 -p32
335 30_ at	Cluster Incl. M33326:Human nonspecific cross-reacting antigen (NCA) mRNA, complete cds /cds=(86,1135) /gb=M33326 /gi=189101 /ug=Hs.41 /len=2287	CEAC AM8	carcinoembryoni c antigen- related cell adhesion molecule 8	19q13. 2
336 89_ s_at	Cluster Incl. AF012434:untitled /cds=(38,394) /gb=AF012434 /gi=2352914 /ug=Hs.186570 /len=573			
337 31_ at	Cluster Incl. AJ130718:Homo sapiens mRNA for glycoprotein-associated amino acid transporter y+LAT1 /cds=(293,1828) /gb=AJ130718 /gi=3970724 /ug=Hs.194693 /len=2214	SLC7A 7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	14q11. 2
337 52_ at	Cluster Incl. AB020657:Homo sapiens mRNA for KIAA0850 protein, complete cds /cds=(630,2558) /gb=AB020657 /gi=4240188 /ug=Hs.197298 /len=3682	NS1- BP	NS1-binding protein	1q25.1 -q31.1

338 12_ at	"Cluster Incl. AL049415:Homo sapiens mRNA; cDNA DKFZp586N2119 (from clone DKFZp586N2119) /cds=UNKNOWN /gb=AL049415 /gi=4500196 /ug=Hs.204290 /len=1232"			
338 21_ at	Cluster Incl. AL034374:Human DNA sequence from clone 483K16 on chromosome 6p12.1-21.1. Contains (parts of) two novel genes, 40S Ribosomal protein S16 and 60S Ribosomal protein L31 pseudogenes, ESTs, STSs, GSSs and a putative CpG island /cds=(0,703) /gb=AL			
338 56_ at	Cluster Incl. Y13374:Homo sapiens mRNA for putatively prenylated protein /cds=(343,972) /gb=Y13374 /gi=2370152 /ug=Hs.239533 /len=1186	CXX1	CAAX box 1	Xq26
338 60_ at	Cluster Incl. AB007931:Homo sapiens mRNA for KIAA0462 protein, partial cds /cds=(0,6831) /gb=AB007931 /gi=3413885 /ug=Hs.239686 /len=7150	KIAA0462	KIAA0462 protein	1p36.13
338 66_ at	Cluster Incl. X05276:Human mRNA for fibroblast tropomyosin TM30 (pl) /cds=(50,796) /gb=X05276 /gi=37201 /ug=Hs.239804 /len=2049	TPM4	tropomyosin 4	19p13.1
339 05_ at	Cluster Incl. AF072242:Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds /cds=(229,1464) /gb=AF072242	MBD2	methyl-CpG binding domain protein 2	18q21

	/gi=3800792 /ug=Hs.25674 /len=1948			
339 20_ at	Cluster Incl. AF051782:Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds /cds=(0,3746) /gb=AF051782 /gi=2947237 /ug=Hs.26584 /len=5635	DIAPH 1	diaphanous (Drosophila, homolog) 1	5q31
339 24_ at	Cluster Incl. AB029014:Homo sapiens mRNA for KIAA1091 protein, partial cds /cds=(0,4080) /gb=AB029014 /gi=5689518 /ug=Hs.26797 /len=4248	KIAA1 091	KIAA1091 protein	11
339 44_ at	Cluster Incl. S60099:APPH=amyloid precursor protein homolog [human, placenta, mRNA, 3727 nt] /cds=(72,2363) /gb=S60099 /gi=300168 /ug=Hs.64797 /len=3727	APLP2	amyloid beta (A4) precursor-like protein 2	11q24
339 63_ at	Cluster Incl. M96326:Human azurocidin gene, complete cds /cds=(16,771) /gb=M96326 /gi=179301 /ug=Hs.72885 /len=913			
341 10_ g_a t	Cluster Incl. AF010310:Homo sapiens p53 induced protein mRNA, partial cds /cds=(0,761) /gb=AF010310 /gi=2415296 /ug=Hs.211605 /len=888	PIG6	proline oxidase homolog	
341 68_ at	Cluster Incl. M11722:Human terminal transferase mRNA, complete cds /cds=(328,1854) /gb=M11722 /gi=339436 /ug=Hs.234772 /len=2068	DNTT	deoxynucleotidyltransferase, terminal	10q23-q24
342 10_ at	Cluster Incl. N90866:zb11b10.s1 Homo sapiens cDNA, 3 end	CDW5 2	CDW52 antigen (CAMPATH-1)	1p36

at	/clone=IMAGE-301723 /clone_end=3 /gb=N90866 /gi=1444193 /ug=Hs.214742 /len=577	2	antigen)	
342 51_ at	Cluster Incl. M92299:Human homeobox 2.1 protein (HOX2A) mRNA, complete cds /cds=(275,1084) /gb=M92299 /gi=184292 /ug=Hs.22554 /len=2037	HOXB 5	homeo box B5	17q21- q22
343 06_ at	Cluster Incl. AB007888:Homo sapiens KIAA0428 mRNA, complete cds /cds=(1414,2526) /gb=AB007888 /gi=2887430 /ug=Hs.28578 /len=5940	MBNL	muscleblind (Drosophila)-like	3q25
343 62_ at	Cluster Incl. M55531:Human glucose transport-like 5 (GLUT5) mRNA, complete cds /cds=(75,1580) /gb=M55531 /gi=183297 /ug=Hs.33084 /len=2218	SLC2A 5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	1p36.2
343 67_ at	Cluster Incl. AF006043:Homo sapiens 3-phosphoglycerate dehydrogenase mRNA, complete cds /cds=(692,2293) /gb=AF006043 /gi=2674061 /ug=Hs.3343 /len=2467	PHGD H	phosphoglycerat e dehydrogenase	1p12
345 12_ at	Cluster Incl. J03853:Human kidney alpha-2-adrenergic receptor mRNA, complete cds /cds=(38,1423) /gb=J03853 /gi=178193 /ug=Hs.123022 /len=1491	ADRA 2C	adrenergic, alpha-2C-, receptor	4p16
345 46_	Cluster Incl. AI250799:qi36g07.x1 Homo sapiens cDNA, 3 end	DEFA4	defensin, alpha 4, corticostatin	8p23

at	/clone=IMAGE-1858620 /clone_end=3 /gb=AI250799 /gi=3847328 /ug=Hs.2582 /len=542		4, corticostatin	
345 83_ at	Cluster Incl. U02687:Human growth factor receptor tyrosine kinase (STK-1) mRNA; complete cds /cds=(57,3038) /gb=U02687 /gi=409572 /ug=Hs.385 /len=3475	FLT3	fms-related tyrosine kinase 3	13q12
346 54_ at	Cluster Incl. AJ224979:Homo sapiens mRNA for MTMR1 protein /cds=(0,1990) /gb=AJ224979 /gi=4128155 /ug=Hs.23200 /len=2582	MTMR 1	myotubularin related protein 1	Xq28
346 63_ at	Cluster Incl. M28696:Human low- affinity IgG Fc receptor (beta-Fc- gamma-RII) mRNA, complete cds /cds=(41,916) /gb=M28696 /gi=184843 /ug=Hs.233450 /len=1416	FCGR 2B	Fc fragment of IgG, low affinity IIb, receptor for (CD32)	1q23
346 70_ at	Cluster Incl. U60899:Human lysosomal alpha-mannosidase (manB) gene /cds=(309,3341) /gb=U60899 /gi=2209014 /ug=Hs.234070 /len=3443			
346 79_ at	Cluster Incl. X02596:Human mRNA for bcr (breakpoint cluster region) gene in Philadelphia chromosome /cds=(488,4303) /gb=X02596 /gi=29420 /ug=Hs.234799 /len=4739	BCR	breakpoint cluster region	22q11. 23
347 80_ at	Cluster Incl. AB002313:Human mRNA for KIAA0315 gene, partial cds /cds=(0,5526) /gb=AB002313 /gi=2280475 /ug=Hs.3989 /len=6252	PLXN B2	plexin B2	22q13. 33

	/gi=2280475 /ug=Hs.3989 /len=6252			
347 85_ at	Cluster Incl. AB028948:Homo sapiens mRNA for KIAA1025 protein, partial cds /cds=(0,3441) /gb=AB028948 /gi=5689386 /ug=Hs.4084 /len=6131	KIAA1025	KIAA1025 protein	12q24.22
347 89_ at	Cluster Incl. S69272:cytoplasmic antiproteinase=38 kda intracellular serine proteinase inhibitor [human, placenta, mRNA, 1465 nt] /cds=(188,1318) /gb=S69272 /gi=546087 /ug=Hs.41072 /len=1465	SERPINB6	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6	6p25
348 30_ at	Cluster Incl. W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	DKFZP564K0822	hypothetical protein DKFZp564K0822	6
348 71_ at	Cluster Incl. W30677:zb75h10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-309475 /clone_end=5 /gb=W30677 /gi=1311730 /ug=Hs.5019 /len=614		Homo sapiens cDNA FLJ11714 fis, clone HEMBA100521 9, weakly similar to NUCLEAR PROTEIN SNF7	
348 92_ at	Cluster Incl. AF016266:Homo sapiens TRAIL receptor 2 mRNA, complete cds /cds=(117,1439) /gb=AF016266 /gi=2529562 /ug=Hs.51233 /len=3972	TNFRSF10B	tumor necrosis factor receptor superfamily, member 10b	8p22-p21
350 16_ at	Cluster Incl. M13560:Human Ia-associated invariant gamma-chain gene /cds=(795,1493) /gb=M13560 /gi=184518 /ug=Hs.84298 /len=2080			

	/gi=184518 /ug=Hs.84298 /len=2080			
350 78_ at	Cluster Incl. X93093:H.sapiens LW gene /cds=(9,824) /gb=X93093 /gi=1491707 /ug=Hs.108287 /len=1243	ICAM4	intercellular adhesion molecule 4, Landsteiner- Wiener blood group	19p13. 2-cen
351 54_ at	Cluster Incl. W68046:zd42a12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-343294 /clone_end=3 /gb=W68046 /gi=1376935 /ug=Hs.25817 /len=575	BTBD2	BTB (POZ) domain containing 2	19p13. 3
352 04_ at	Cluster Incl. U52840:Homo sapiens semaphorin F homolog mRNA, complete cds /cds=(637,3861) /gb=U52840 /gi=2772583 /ug=Hs.27621 /len=8056	SEMA 5A	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	5p15.2
352 30_ at	Cluster Incl. AF070530:Homo sapiens clone 24751 unknown mRNA /cds=(0,1252) /gb=AF070530 /gi=3387885 /ug=Hs.29344 /len=1560	CL247 51	hypothetical protein, clone 24751	19p13. 3
352 60_ at	Cluster Incl. AB020674:Homo sapiens mRNA for KIAA0867 protein, complete cds /cds=(152,1732) /gb=AB020674	MOND OA	KIAA0867 protein	12q21. 31

at	/gi=4240222 /ug=Hs.52081 /len=4339			
352 64_ at	Cluster Incl. AF067139:Homo sapiens NADH-ubiquinone oxidoreductase NDUF S3 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds /cds=(12,806) /gb=AF067139 /gi=3337440 /ug=Hs.5273 /len=887	NDUF S3	NADH dehydrogenase (ubiquinone) Fe-S protein 3 (30kD) (NADH-coenzyme Q reductase)	11p11.11
352 82_ r_at	Cluster Incl. M33680:Human 26-kDa cell surface protein TAPA-1 mRNA, complete cds /cds=(238,948) /gb=M33680 /gi=338677 /ug=Hs.54457 /len=1480	CD81	CD81 antigen (target of antiproliferative antibody 1)	11p15
353 29_ at	Cluster Incl. AF091084:Homo sapiens clone 638 unknown mRNA, complete sequence /cds=(30,413) /gb=AF091084 /gi=3860005 /ug=Hs.5825 /len=1065	LOC51706	cytochrome b5 reductase 1 (B5R.1)	1p36.13-q41
353 40_ at	Cluster Incl. A1819948:wj88e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2409932 /clone_end=3 /gb=A1819948 /gi=5439027 /ug=Hs.5947 /len=569	MEL	mel transforming oncogene (derived from cell line NK14)-RAB8 homolog	19p13.1
353 50_ at	Cluster Incl. AB011170:Homo sapiens mRNA for KIAA0598 protein, complete cds /cds=(581,2266) /gb=AB011170 /gi=3043719 /ug=Hs.6079 /len=4712	GALN AC4S-6ST	B cell RAG associated protein	10q26
353 55_	Cluster Incl. AB020697:Homo sapiens mRNA for KIAA0890 protein, complete	DDX30	DEAD/H (Asp-Glu-Ala-	3p21.31

at	cds /cds=(143,3727) /gb=AB020697 /gi=4240268 /ug=Hs.6141 /len=3800		Asp/His) box polypeptide 30	1
353 72_ r_at	Cluster Incl. M17017:Human beta-thromboglobulin-like protein mRNA, complete cds /cds=(90,389) /gb=M17017 /gi=179579 /ug=Hs.624 /len=1639	IL8	interleukin 8	4q13-q21
356 38_ at	Cluster Incl. D43638:Human mRNA for MTG8a protein, complete cds /cds=(411,2144) /gb=D43638 /gi=940399 /ug=Hs.31551 /len=3460	CBFA2 T1	"core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related"	8q22
356 43_ at	Cluster Incl. X76732:H.sapiens mRNA for NEFA protein /cds=(219,1481) /gb=X76732 /gi=2706486 /ug=Hs.3164 /len=1586	NUCB 2	nucleobindin 2	11p15.1-p14
357 66_ at	Cluster Incl. M26326:Human keratin 18 mRNA, complete cds /cds=(51,1343) /gb=M26326 /gi=186690 /ug=Hs.65114 /len=1412	KRT18	keratin 18	12q13
358 13_ at	Cluster Incl. AA192359:zp91c12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-627574 /clone_end=3 /gb=AA192359 /gi=1781699 /ug=Hs.69235 /len=715	TRN-SR	transportin-SR	7q32.2-q32.3
358 23_ at	Cluster Incl. M63573:Human secreted cyclophilin-like protein (SCYLP) mRNA, complete cds /cds=(21,671)	PPIB	peptidylprolyl isomerase B (cyclophilin B)	15q21-q22

at	/gb=M63573 /gi=337998 /ug=Hs.699 /len=893		(cyclophilin B)	
359 19_ at	Cluster Incl. J05068:human transcobalamin I mRNA, complete cds /cds=(75,1376) /gb=J05068 /gi=307478 /ug=Hs.2012 /len=1537	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	11q11- q12
359 39_ s_at	Cluster Incl. L20433:Human octamer binding transcription factor 1 (OTF1) mRNA, complete cds /cds=(234,1496) /gb=L20433 /gi=418015 /ug=Hs.211588 /len=3824	POU4 F1	POU domain, class 4, transcription factor 1	13q21. 1-q22
359 40_ at	Cluster Incl. X64624:H.sapiens mRNA for RDC-1 POU domain containing protein /cds=(277,1272) /gb=X64624 /gi=35914 /ug=Hs.211588 /len=3492	POU4 F1	POU domain, class 4, transcription factor 1	13q21. 1-q22
359 41_ f_at	Cluster Incl. U91329:Human kinesin- like motor protein KIF1C mRNA, complete cds /cds=(113,3424) /gb=U91329 /gi=2738148 /ug=Hs.211611 /len=4058	KIF1C	kinesin family member 1C	17p13
359 95_ at	Cluster Incl. AF067656:Homo sapiens ZW10 interactor Zwint mRNA, complete cds /cds=(24,857) /gb=AF067656 /gi=3901271 /ug=Hs.42650 /len=1639	ZWINT	ZW10 interactor	10q21- q22
360 21_ at	"Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN /gb=AL049409			

	/gi=4500194 /ug=Hs.44865 /len=1419"			
360 95_ at	Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE- 20074 /gb=N99340 /gi=1270755 /ug=Hs.7357 /len=1110	DKFZ P586N 1922	DKFZP586N192 2 protein	19q13. 1
361 03_ at	Cluster Incl. D90144:Homo sapiens gene for LD78 alpha precursor, complete cds /cds=(86,364) /gb=D90144 /gi=219905 /ug=Hs.73817 /len=781	SCYA 3	small inducible cytokine A3 (homologous to mouse Mip-1a)	17q11- q21
361 23_ at	Cluster Incl. D87292:Homo sapiens mRNA for rhodanese, complete cds /cds=(48,941) /gb=D87292 /gi=1877030 /ug=Hs.74097 /len=1137	TST	thiosulfate sulfurtransferas e (rhodanese)	22q13. 1
361 39_ at	"Cluster Incl. AL050289:Homo sapiens mRNA; cDNA DKFZp586G0522 (from clone DKFZp586G0522) /cds=(179,1876) /gb=AL050289 /gi=4886510 /ug=Hs.7446 /len=2364"	C6orf5	chromosome 6 open reading frame 5	6q21
361 55_ at	Cluster Incl. D87465:Human mRNA for KIAA0275 gene, complete cds /cds=(316,1590) /gb=D87465 /gi=1665814 /ug=Hs.74583 /len=5316	KIAA0 275	KIAA0275 gene product	10pter- q25.3
361 65_ at	Cluster Incl. W51774:zc48b04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-325519 /clone_end=5 /gb=W51774 /gi=1349666 /ug=Hs.74649 /len=678	COX6 C	cytochrome c oxidase subunit VIc	8q22- q23

361 _at	Y13620 /FEATURE= /DEFINITION=HSRNABCL9 Homo sapiens mRNA for BCL9 gene	BCL9	B-cell CLL/lymphoma 9	1q21
362 39_ at	Cluster Incl. Z49194:H.sapiens mRNA for oct-binding factor /cds=(523,1293) /gb=Z49194 /gi=974830 /ug=Hs.2407 /len=3301	POU2 AF1	POU domain, class 2, associating factor 1	11q23. 1
364 64_ at	Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213612 /ug=Hs.54431 /len=2124	SGP28	specific granule protein (28 kDa)	6p12.3
365 36_ at	Cluster Incl. AF070614:Homo sapiens clone 24732 unknown mRNA, partial cds /cds=(0,1147) /gb=AF070614 /gi=3283878 /ug=Hs.61490 /len=1734	SCHIP 1	schwannomin- interacting protein 1	3q26.1
365 53_ at	Cluster Incl. AA669799:ag36c04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1118886 /clone_end=3 /gb=AA669799 /gi=2631298 /ug=Hs.6315 /len=679	ASMT L	acetylserotonin O- methyltransfera se-like	Xp22.3
365 71_ at	Cluster Incl. X68060:H.sapiens topIIB mRNA for topoisomerase IIB /cds=(0,4865) /gb=X68060 /gi=37230 /ug=Hs.75248 /len=4866	TOP2 B	topoisomerase (DNA) II beta (180kD)	3p24
365 88_ at	Cluster Incl. AB018353:Homo sapiens mRNA for KIAA0810 protein, partial cds /cds=(0,2475) /gb=AB018353 /gi=3882340 /ug=Hs.7531 /len=4047	KIAA0 810	KIAA0810 protein	

366 01_ at	Cluster Incl. M33308:Human vinculin mRNA, complete cds /cds=(50,3250) /gb=M33308 /gi=340236 /ug=Hs.75350 /len=5102	VCL	vinculin	10q22.1-q23
366 07_ at	Cluster Incl. Z99716:bK250D10.5 (alpha-N-acetylgalactosaminidase) /cds=(472,1707) /gb=Z99716 /gi=4456457 /ug=Hs.75372 /len=3606			
366 08_ at	Cluster Incl. D55654:Human mRNA for cytosolic malate dehydrogenase, complete cds /cds=(55,1059) /gb=D55654 /gi=1255603 /ug=Hs.75375 /len=1267	MDH1	malate dehydrogenase 1, NAD (soluble)	2p16
366 29_ at	Cluster Incl. A1635895:tz82a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2295060 /clone_end=3 /gb=A1635895 /gi=4687225 /ug=Hs.75450 /len=1082	DSIPI	delta sleep inducing peptide, immunoreactor	Xp21.1-q25
366 38_ at	Cluster Incl. X78947:H.sapiens mRNA for connective tissue growth factor /cds=(145,1194) /gb=X78947 /gi=474933 /ug=Hs.75511 /len=2312	CTGF	connective tissue growth factor	6q23.1
366 44_ at	Cluster Incl. D29963:Homo sapiens mRNA for CD151, complete cds /cds=(84,845) /gb=D29963 /gi=2073384 /ug=Hs.75564 /len=1486	CD151	CD151 antigen	11p15.5
366 61_ s_at	Cluster Incl. X06882:Human gene for CD14 differentiation antigen /cds=(105,1232) /gb=X06882 /gi=29736 /ug=Hs.75627 /len=1356	CD14	CD14 antigen	5q31.1

	/gi=29736 /ug=Hs.75627 /len=1356			
366 67_ at	Cluster Incl. U47025:Human fetal brain glycogen phosphorylase B mRNA, complete cds /cds=(34,2565) /gb=U47025 /gi=1172225 /ug=Hs.75658 /len=4055	PYGB	"phosphorylase, glycogen; brain"	20p11.2-p11.1
366 90_ at	Cluster Incl. M10901:Human glucocorticoid receptor alpha mRNA, complete cds /cds=(132,2465) /gb=M10901 /gi=183032 /ug=Hs.75772 /len=4788	NR3C1	nuclear receptor subfamily 3, group C, member 1	5q31
367 09_ at	Cluster Incl. Y00093:H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95 /cds=(64,3555) /gb=Y00093 /gi=35175 /ug=Hs.51077 /len=4654	ITGAX	integrin, alpha X (antigen CD11C (p150), alpha polypeptide)	16p11.2
367 10_ at	Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	CAMP	cathelicidin antimicrobial peptide	3p21.3
367 49_ at	Cluster Incl. M73720:Human mast cell carboxypeptidase A (MC-CPA) gene /cds=(11,1264) /gb=M73720 /gi=187441 /ug=Hs.646 /len=1633			
367 66_ at	Cluster Incl. X55988:Human EDN mRNA for eosinophil derived neurotoxin /cds=(71,556) /gb=X55988 /gi=31088 /ug=Hs.728 /len=735	RNAS E2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	14q24-q31

367 73_ f_at	Cluster Incl. M81141:Human MHC class II HLA-DQ-beta mRNA (DR7 DQw2), complete cds /cds=(35,820) /gb=M81141 /gi=188202 /ug=Hs.73933 /len=1171	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	6p21.3
367 90_ at	Cluster Incl. M19267:Human tropomyosin mRNA, complete cds /cds=(286,1140) /gb=M19267 /gi=339943 /ug=Hs.77899 /len=1633	TPM1	tropomyosin 1 (alpha)	15q22.1
367 98_ g_a t	Cluster Incl. J04168:Human leukosialin mRNA, complete cds /cds=(95,1297) /gb=J04168 /gi=187118 /ug=Hs.80738 /len=2288	SPN	sialophorin (gpL115, leukosialin, CD43)	16p11.2
368 02_ at	Cluster Incl. M23197:Human differentiation antigen (CD33) mRNA, complete cds /cds=(12,1106) /gb=M23197 /gi=180097 /ug=Hs.83731 /len=1437	CD33	CD33 antigen (gp67)	19q13.3
368 09_ at	Cluster Incl. L01664:Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) mRNA, complete cds /cds=(33,461) /gb=L01664 /gi=187273 /ug=Hs.889 /len=586	CLC	Charot-Leyden crystal protein	19q13.1
368 43_ at	Cluster Incl. AB005666:Homo sapiens mRNA for GTPase-activating protein, complete cds /cds=(296,3424) /gb=AB005666 /gi=2389008 /ug=Hs.7019 /len=3885	SIPA1	signal-induced proliferation-associated gene 1	11q13.3
368 73_	Cluster Incl. D16532:Human gene for very low density lipoprotein receptor,			

at	5flanking and /cds=(615,3236) /gb=D16532 /gi=407220 /ug=Hs.73729 /len=3853			
368 78_ f_at	Cluster Incl. M60028:Human MHC class II HLA-DQ-beta (DQB1,DQw9), complete cds /cds=(57,842) /gb=M60028 /gi=188114 /ug=Hs.73931 /len=1192	HLA- DQB1	major histocompatibilit y complex, class II, DQ beta 1	6p21.3
368 81_ at	Cluster Incl. X71129:H.sapiens mRNA for electron transfer flavoprotein beta subunit /cds=(27,794) /gb=X71129 /gi=297901 /ug=Hs.74047 /len=835	ETFB	electron- transfer- flavoprotein, beta polypeptide	19q13. 3
368 94_ at	Cluster Incl. AL031846:dJ742C19.5 (novel Chromobox protein) /cds=(89,844) /gb=AL031846 /gi=4164368 /ug=Hs.7442 /len=3964			
369 00_ at	Cluster Incl. U52426:Homo sapiens GOK (STIM1) mRNA, complete cds /cds=(565,2622) /gb=U52426 /gi=2264345 /ug=Hs.74597 /len=4040.	STIM1	stromal interaction molecule 1	11p15. 5
369 36_ at	Cluster Incl. U58766:Human FX protein mRNA, complete cds /cds=(74,1039) /gb=U58766 /gi=1381178 /ug=Hs.75801 /len=1330	TSTA3	tissue specific transplantation antigen P35B	8q24.3
369 45_ at	Cluster Incl. X94910:Homo sapiens mRNA for ERp28 protein /cds=(11,796) /gb=X94910 /gi=3413292 /ug=Hs.75841 /len=892	C12orf 8	chromosome 12 open reading frame 8	12q24. 13

369 52_ at	Cluster Incl. D16480:Homo sapiens mRNA for mitochondrial enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of trifunctional protein, complete cds /cds=(27,2318) /gb=D16480 /gi=493657 /ug=Hs.75860 /len=2690	HADH A	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit	2p23
369 63_ at	Cluster Incl. U30255:Human phosphogluconate dehydrogenase (hPGDH) gene, complete cds /cds=(6,1457) /gb=U30255 /gi=984324 /ug=Hs.75888 /len=1536	PGD	phosphogluconate dehydrogenase	1p36.3 - p36.13
369 73_ at	Cluster Incl. U41371:Human spliceosome associated protein (SAP 145) mRNA, complete cds /cds=(48,2666) /gb=U41371 /gi=1173904 /ug=Hs.75916 /len=2820	SF3B2	splicing factor 3b, subunit 2, 145kD	11q13.1
369 80_ at	Cluster Incl. U03105:Human B4-2 protein mRNA, complete cds /cds=(113,1096) /gb=U03105 /gi=476094 /ug=Hs.75969 /len=2061	B4-2	proline-rich protein with nuclear targeting signal	6q16.1
369 96_ at	Cluster Incl. U41635:Human OS-9 precursor mRNA, complete cds /cds=(85,2088) /gb=U41635 /gi=1322233 /ug=Hs.76228 /len=2736	OS-9	amplified in osteosarcoma	12q13
370 01_	Homo sapiens /REF=M23254 /DEF=Cluster Incl. :Human Ca2-	CAPN 2	calpain 2, (m/II) large subunit	1q41-q42

at	activated neutral protease large subunit (CANP) mRNA, complete cds /cds=(130,2232) /gb= /gi=511636 /ug=Hs.76288 /len=3213 /LEN=3435	2	large subunit	q42
370 15_ at	Cluster Incl. K03000:Human aldehyde dehydrogenase 1 mRNA /cds=(0,1022) /gb=K03000 /gi=178399 /ug=Hs.76392 /len=1560	ALDH1 A1	aldehyde dehydrogenase 1 family, member A1	9q21
370 18_ at	Cluster Incl. A189287:qd05c04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1722822 /clone_end=3 /gb=A189287 /gi=3740496 /ug=Hs.7644 /len=738	H1F2	H1 histone family, member 2	6p21.3
370 21_ at	Cluster Incl. X16832:Human mRNA for cathepsin H (EC 3.4.22.16) /cds=(34,1041) /gb=X16832 /gi=29709 /ug=Hs.76476 /len=1399	CTSH	cathepsin H	15q24-q25
370 23_ at	Cluster Incl. J02923:Human 65-kilodalton phosphoprotein (p65) mRNA, complete cds /cds=(74,1957) /gb=J02923 /gi=189501 /ug=Hs.76506 /len=3175	LCP1	lymphocyte cytosolic protein 1 (L-plastin)	13q14.3
370 26_ at	Cluster Incl. AF001461:Homo sapiens Kruppel-like zinc finger protein Zf9 mRNA, complete cds /cds=(30,881) /gb=AF001461 /gi=3378030 /ug=Hs.76526 /len=1354	COPE B	core promoter element binding protein	10p15
370 27_ at	Cluster Incl. M80899:Human novel protein AHNAK mRNA, partial sequence /cds=(0,3835) /gb=M80899	AHNA K	AHNAK nucleoprotein (desmoyokin)	11q12-q13

at	/gi=178282 /ug=Hs.76549 /len=4051		(desmoyokin)	
370 29_ at	Homo sapiens /REF=X83218 /DEF=Cluster Incl. :H.sapiens mRNA for ATP synthase /cds=(36,677) /gb= /gi=1008079 /ug=Hs.76572 /len=750 /LEN=826	ATP5 O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein)	21q22. 11
370 39_ at	Cluster Incl. J00194:human hla-dr antigen alpha-chain mrna & ivs fragments /cds=(26,790) /gb=J00194 /gi=188231 /ug=Hs.76807 /len=1199	HLA- DRA	major histocompatibilit y complex, class II, DR alpha	6p21.3
370 54_ at	Cluster Incl. J04739:Human bactericidal permeability increasing protein (BPI) mRNA, complete cds /cds=(30,1493) /gb=J04739 /gi=179528 /ug=Hs.89535 /len=1813	BPI	bactericidal/per meability- increasing protein	20q11. 23-q12
370 99_ at	Cluster Incl. A1806222:wf26e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2356746 /clone_end=3 /gb=A1806222 /gi=5392788 /ug=Hs.100194 /len=563	ALOX5 AP	arachidonate 5- lipoxygenase- activating protein	13q12
371 47_ at	Cluster Incl. AF020044:Homo sapiens lymphocyte secreted C-type lectin precursor, mRNA, complete cds /cds=(179,1150) /gb=AF020044 /gi=2828595 /ug=Hs.105927 /len=1391	SCGF	"stem cell growth factor; lymphocyte secreted C-type lectin"	19q13. 3

371 49_ s_at	Cluster Incl. U95626:Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds /cds=(2,1429) /gb=U95626 /gi=2104517 /ug=Hs.105938 /len=1607			
371 59_ at	Cluster Incl. U79259:Human clone 23945 mRNA, complete cds /cds=(636,1403) /gb=U79259 /gi=1710213 /ug=Hs.10700 /len=1683	DJ159 A19.3	hypothetical protein	1p36.1 3
372 63_ at	Cluster Incl. U55206:Homo sapiens human gamma-glutamyl hydrolase (hGH) mRNA, complete cds /cds=(59,1015) /gb=U55206 /gi=2957143 /ug=Hs.78619 /len=1265	GGH	gamma- glutamyl hydrolase (conjugase, folylpolygamma glutamyl hydrolase)	8q12.1
373 11_ at	Cluster Incl. AF010400:untitled /cds=(50,1063) /gb=AF010400 /gi=2612878 /ug=Hs.77290 /len=1242			
373 26_ at	"Cluster Incl. U93305:Homo sapiens A4 differentiation-dependent protein (A4), triple LIM domain protein (LMO6), and synaptophysin (SYP) genes, complete cds; and calcium channel alpha-1 subunit (CACNA1F) gene, partial cds /cds=(75,533) /gb=U93305 /gi=270759"			
373 33_ at	Cluster Incl. X63692:H.sapiens mRNA for DNA (cytosine-5)-methyltransferase /cds=(237,5087) /gb=X63692	DNMT 1	DNA (cytosine- 5-)- methyltransfera	19p13. 2

at	/gi=1632818 /ug=Hs.77462 /len=5408		se 1	
373 44_ at	Cluster Incl. X62744:Human RING6 mRNA for HLA class II alpha chain-like product /cds=(45,830) /gb=X62744 /gi=36062 /ug=Hs.77522 /len=1079	HLA-DMA	major histocompatibility complex, class II, DM alpha	6p21.3
373 84_ at	Cluster Incl. D13640:Human mRNA for KIAA0015 gene, complete cds /cds=(106,1470) /gb=D13640 /gi=286006 /ug=Hs.77961 /len=5134	KIAA0015	KIAA0015 gene product	22q11.22
373 99_ at	Cluster Incl. D17793:Human mRNA for KIAA0119 gene, complete cds /cds=(51,1022) /gb=D17793 /gi=457407 /ug=Hs.78183 /len=1204	AKR1C3	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)	10p15-p14
374 03_ at	Cluster Incl. X05908:Human mRNA for lipocortin /cds=(74,1114) /gb=X05908 /gi=34387 /ug=Hs.78225 /len=1399	ANXA1	annexin A1	9q12-q21.2
374 07_ s_at	Cluster Incl. AF013570:Homo sapiens smooth muscle myosin heavy chain SM2 mRNA, alternatively spliced, partial cds /cds=(0,1767) /gb=AF013570 /gi=2352944 /ug=Hs.78344 /len=2580	MYH11	myosin, heavy polypeptide 11, smooth muscle	16p13.13-p13.12
374 08_ at	Cluster Incl. AB014609:Homo sapiens mRNA for KIAA0709 protein, complete cds /cds=(116,4555) /gb=AB014609 /gi=3327231 /ug=Hs.7835 /len=5641	KIAA0709	endocytic receptor (macrophage mannose receptor family)	17q24.1

			receptor family)	
374 17_ at	Cluster Incl. M36542:Human lymphoid-specific transcription factor mRNA, complete cds /cds=(54,1445) /gb=M36542 /gi=339495 /ug=Hs.1101 /len=2048	POU2 F2	POU domain, class 2, transcription factor 2	19q13.31
375 79_ at	Cluster Incl. L47738:Homo sapiens inducible protein mRNA, complete cds /cds=(1004,1714) /gb=L47738 /gi=1009098 /ug=Hs.80313 /len=2881	PIR12 1	cytoplasmic FMRP interacting protein 2	5q34
376 00_ at	Cluster Incl. U68186:Human extracellular matrix protein 1 mRNA, complete cds /cds=(103,1725) /gb=U68186 /gi=2660683 /ug=Hs.81071 /len=1819	ECM1	extracellular matrix protein 1	1q21
376 15_ at	Cluster Incl. D86962:Human mRNA for KIAA0207 gene, complete cds /cds=(781,2547) /gb=D86962 /gi=1503997 /ug=Hs.81875 /len=5431	GRB1 0	growth factor receptor-bound protein 10	7p12-p11.2
376 25_ at	Cluster Incl. U52682:Human lymphocyte specific interferon regulatory factor/interferon regulatory factor 4 (LSIRF/IRF4) mRNA, complete cds /cds=(125,1477) /gb=U52682 /gi=1378108 /ug=Hs.82132 /len=5320	IRF4	interferon regulatory factor 4	6p25-p23
376 57_ at	Cluster Incl. Y16270:Homo sapiens PALM gene, exon 1 and joined CDS /cds=(145,1308) /gb=Y16270 /gi=3219601 /ug=Hs.78482 /len=2823			

376 69_ s_at	Cluster Incl. U16799:Human Na,K-ATPase beta-1 subunit mRNA, complete cds /cds=(45,950) /gb=U16799 /gi=806753 /ug=Hs.78629 /len=1476	ATP1B 1	ATPase, Na+/K+ transporting, beta polypeptide 1	1q22-q25
377 01_ at	Cluster Incl. L13463:Human helix-loop-helix basic phosphoprotein (G0S8) mRNA, complete cds /cds=(32,667) /gb=L13463 /gi=292054 /ug=Hs.78944 /len=1345	RGS2	regulator of G-protein signalling 2, 24kD	1q31
377 39_ at	Cluster Incl. M86737:Human high mobility group box (SSRP1) mRNA, complete cds /cds=(274,2403) /gb=M86737 /gi=184241 /ug=Hs.79162 /len=2825	SSRP 1	structure specific recognition protein 1	11q12
377 47_ at	Cluster Incl. U05770:Human annexin V (ANX5) gene /cds=(164,1126) /gb=U05770 /gi=2182176 /ug=Hs.79274 /len=1597			
377 55_ at	Cluster Incl. AB023169:Homo sapiens mRNA for KIAA0952 protein, complete cds /cds=(359,1927) /gb=AB023169 /gi=4589547 /ug=Hs.7935 /len=4856	KIAA0952	KIAA0952 protein	20p12.1
377 62_ at	Cluster Incl. Y07909:H.sapiens mRNA for Progression Associated Protein 1 /cds=(218,691) /gb=Y07909 /gi=1542882 /ug=Hs.79368 /len=2774	EMP1	epithelial membrane protein 1	12p12.3
377 75_	Cluster Incl. W25951:17d10 Homo sapiens cDNA /gb=W25951		septin 6	Xq24

at	/gi=1306236 /ug=Hs.123282 /len=738			
378 09_ at	Cluster Incl. U41813:Human class I homeoprotein (HOXA9) mRNA, partial cds /cds=(0,389) /gb=U41813 /gi=1184168 /ug=Hs.127428 /len=1411	HOXA 9	homeo box A9	7p15- p14
378 11_ at	Cluster Incl. AF042792:Homo sapiens alpha 2 delta calcium channel subunit isoform .1 mRNA, complete cds /cds=(161,3598) /gb=AF042792 /gi=2781438 /ug=Hs.127436 /len=5463	CACN A2D2	calcium channel, voltage- dependent, alpha 2/delta subunit 2	3p21.3
378 97_ s_at	Cluster Incl. AI985964:wr79d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2493903 /clone_end=3 /gb=AI985964 /gi=5813241 /ug=Hs.82961 /len=487	TFF3	trefoil factor 3 (intestinal)	21q22. 3
379 26_ at	Cluster Incl. D14520:Human mRNA for GC-Box binding protein BTEB2, complete cds /cds=(558,1217) /gb=D14520 /gi=303596 /ug=Hs.84728 /len=1301	KLF5	Kruppel-like factor 5 (intestinal)	13q21. 32
379 54_ at	Cluster Incl. X16662:Human mRNA for vascular anticoagulant-beta (VAC-beta) /cds=(106,1089) /gb=X16662 /gi=37638 /ug=Hs.87268 /len=1940	ANXA 8	annexin A8	10q11. 2
379 67_ at	Cluster Incl. AF000424:Homo sapiens LST1 mRNA, cLST1/C splice variant, complete cds /cds=(225,500) /gb=AF000424 /gi=2145063	LY117	lymphocyte antigen 117	6p21.3

	/ug=Hs.88411 /len=635			
379 92_ s_at	Cluster Incl. AI436567:ti03b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2129369 /clone_end=3 /gb=AI436567 /gi=4282731 /ug=Hs.89761 /len=680	ATP5D	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit	19p13. 3
380 06_ at	Cluster Incl. M37766:Human MEM-102 glycoprotein mRNA, complete cds /cds=(20,751) /gb=M37766 /gi=187518 /ug=Hs.901 /len=1058	CD48	CD48 antigen (B-cell membrane protein)	1q21.3 -q22
380 17_ at	Cluster Incl. U05259:Human MB-1 gene, complete cds /cds=(36,716) /gb=U05259 /gi=452561 /ug=Hs.79630 /len=1107			
380 37_ at	Cluster Incl. M60278:Human heparin- binding EGF-like growth factor mRNA, complete cds /cds=(261,887) /gb=M60278 /gi=183866 /ug=Hs.799 /len=2342	DTR	diphtheria toxin receptor (heparin-binding epidermal growth factor- like growth factor)	5q23
380 63_ at	Cluster Incl. U00952:Human clone A9A2BRB7 (CAC) _n /(GTG) _n repeat- containing mRNA /cds=UNKNOWN /gb=U00952 /gi=405054 /ug=Hs.8068 /len=1047			
380 95_ _at	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478	HLA- DPB1	major histocompatibilit y complex, class II, DP beta 1	6p21.3

	/ug=Hs.814 /len=1501		II, DP beta 1	
380 96_ f_at	Cluster Incl. M83664:Human MHC class II lymphocyte antigen (HLA-DP) beta chain mRNA, complete cds /cds=(59,835) /gb=M83664 /gi=188478 /ug=Hs.814 /len=1501	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	6p21.3
380 97_ at	Cluster Incl. AF010313:Homo sapiens Pig8 (PIG8) mRNA, complete cds /cds=(72,1028) /gb=AF010313 /gi=2415301 /ug=Hs.8141 /len=2165	PIG8	etoposide-induced mRNA	11q24
381 12_ g_a t	"Cluster Incl. X15998:H.sapiens mRNA for the chondroitin sulphate proteoglycan versican, V1 splice-variant; precursor peptide /cds=(266,7495) /gb=X15998 /gi=37662 /ug=Hs.81800 /len=8224"	CSPG 2	chondroitin sulfate proteoglycan 2 (versican)	5q14.3
381 16_ at	Cluster Incl. D14657:Human mRNA for KIAA0101 gene, complete cds /cds=(61,396) /gb=D14657 /gi=285938 /ug=Hs.81892 /len=836	KIAA0101	KIAA0101 gene product	15q22.1
381 47_ at	Cluster Incl. AL023657:Homo sapiens SH2D1A cDNA, formerly known as DSHP /cds=(299,685) /gb=AL023657 /gi=3153107 /ug=Hs.151544 /len=2530	SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	Xq25-q26
381 94_ s_at	Cluster Incl. M63438:Human Ig rearranged gamma chain mRNA, V-J-C region and complete cds /cds=(0,1049) /gb=M63438 /gi=184847	IGKC	immunoglobulin kappa constant	2p12

	/ug=Hs.156110 /len=1244			
382 25_ at	Cluster Incl. AF052728:Homo sapiens HERG-USO (HERG) mRNA, alternatively spliced, partial cds /cds=(0,284) /gb=AF052728 /gi=3549258 /ug=Hs.165664 /len=767	KCNH 2	potassium voltage-gated channel, subfamily H (eag-related), member 2	7q35- q36
382 33_ at	Cluster Incl. AF093265:Homo sapiens homer-3 mRNA, complete cds /cds=(90,1166) /gb=AF093265 /gi=3834620 /ug=Hs.166146 /len=1407	HOME R-3	Homer, neuronal immediate early gene, 3	19p13. 12
382 69_ at	"Cluster Incl. AL050147:Homo sapiens mRNA; cDNA DKFZp586E0820 (from clone DKFZp586E0820) /cds=(0,1630) /gb=AL050147 /gi=4884153 /ug=Hs.91146 /len=1837"	PKD2	protein kinase D2	19q13. 2
383 12_ at	"Cluster Incl. AL050002:Homo sapiens mRNA; cDNA DKFZp564O222 (from clone DKFZp564O222) /cds=UNKNOWN /gb=AL050002 /gi=4884256 /ug=Hs.94795 /len=1546"			
383 19_ at	Cluster Incl. AA919102:ol84h02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1536339 /clone_end=3 /gb=AA919102 /gi=3058992 /ug=Hs.95327 /len=622	CD3D	CD3D antigen, delta polypeptide (TIT3 complex)	11q23
383 36_ at	Cluster Incl. AB023230:Homo sapiens mRNA for KIAA1013 protein, partial cds /cds=(0,3188) /gb=AB023230 /gi=4589675 /ug=Hs.96427 /len=4783	KIAA1 013	KIAA1013 protein	3

	/gi=4589675 /ug=Hs.96427 /len=4783			
383 61_ g_a t	Cluster Incl. AI688812:wd41c03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2330692 /clone_end=3 /gb=AI688812 /gi=4900106 /ug=Hs.99491 /len=504	RASG RP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	11q13
383 91_ at	Cluster Incl. M94345:Homo sapiens macrophage capping protein mRNA, complete cds /cds=(49,1095) /gb=M94345 /gi=187455 /ug=Hs.82422 /len=1221	CAPG	capping protein (actin filament), gelsolin-like	2cen- q24
384 14_ at	Cluster Incl. U05340:Human p55CDC mRNA, complete cds /cds=(110,1609) /gb=U05340 /gi=468031 /ug=Hs.82906 /len=1686	CDC2 0	CDC20 (cell division cycle 20, S. cerevisiae, homolog)	9q13- q21
384 15_ at	Cluster Incl. U14603:Human protein- tyrosine phosphatase (HU-PP-1) mRNA, partial sequence /cds=(423,926) /gb=U14603 /gi=894158 /ug=Hs.82911 /len=1526	PTP4A 2	protein tyrosine phosphatase type IVA, member 2	1p35
384 35_ at	Cluster Incl. U25182:Human antioxidant enzyme AOE37-2 mRNA, complete cds /cds=(43,858) /gb=U25182 /gi=799380 /ug=Hs.83383 /len=921	PRDX 4	peroxiredoxin 4	Xp22.1 3
384 65_ at	Cluster Incl. M37721:Human peptidylglycine alpha-amidating monooxygenase mRNA, complete cds /cds=(188,3112) /gb=M37721	PAM	peptidylglycine alpha-amidating monooxygenase	5q14- q21

	/gi=189594 /ug=Hs.83920 /len=3748			
384 72_ at	Cluster Incl. D63477:Human mRNA for KIAA0143 gene, partial cds /cds=(0,2658) /gb=D63477 /gi=1469867 /ug=Hs.84087 /len=5286	KIAA0143	KIAA0143 protein	8q24.2 2
384 85_ at	Cluster Incl. AA760866:nz14h07.s1 Homo sapiens cDNA /clone=IMAGE-1287805 /gb=AA760866 /gi=2809796 /ug=Hs.84549 /len=553	NDUF C1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (6kD, KFYI)	4q28.2 -q31.1
384 87_ at	Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777			
385 77_ at	Cluster Incl. U92981:Homo sapiens clone DT1P1B6 mRNA, CAG repeat region /cds=UNKNOWN /gb=U92981 /gi=2781399 /ug=Hs.18081 /len=1429			
385 78_ at	Cluster Incl. M63928:Homo sapiens T cell activation antigen (CD27) mRNA, complete cds /cds=(100,882) /gb=M63928 /gi=180084 /ug=Hs.180841 /len=1204	TNFR SF7	tumor necrosis factor receptor superfamily, member 7	12p13
386 53_ at	Cluster Incl. D11428:Homo sapiens mRNA for PMP-22(PAS-II/SR13/Gas-3), complete cds /cds=(188,670) /gb=D11428 /gi=220009 /ug=Hs.103724 /len=1806	PMP22	peripheral myelin protein 22	17p12- p11.2

386 66_ at	Cluster Incl. M85169:Human homologue of yeast sec7 mRNA, complete cds /cds=(69,1265) /gb=M85169 /gi=338001 /ug=Hs.1050 /len=3301	PSCD 1	pleckstrin homology, Sec7 and coiled/coil domains 1(cytohesin 1)	17q25
386 95_ at	Cluster Incl. AA203303:zx55b01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446377 /clone_end=5 /gb=AA203303 /gi=1799194 /ug=Hs.10758 /len=876	NDUF S4	NADH dehydrogenase (ubiquinone) Fe- S protein 4 (18kD) (NADH- coenzyme Q reductase)	5q11.1 *
387 05_ at	Cluster Incl. AI310002:qo77c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1914548 /clone_end=3 /gb=AI310002 /gi=4004873 /ug=Hs.108332 /len=656	UBE2 D2	ubiquitin- conjugating enzyme E2D 2 (homologous to yeast UBC4/5)	5p14.2 -q23.3
387 28_ at	Cluster Incl. D86978:Human mRNA for KIAA0225 gene, partial cds /cds=(0,6043) /gb=D86978 /gi=1504029 /ug=Hs.84790 /len=6237	KIAA0 225	KIAA0225 protein	7q33
387 30_ at	Homo sapiens /REF=AB020671 /DEF=Cluster Incl. : mRNA for KIAA0864 protein, partial cds /cds=(0,3656) /gb= /gi=4240216 /ug=Hs.84883 /len=4319 /LEN=4481	KIAA0 864	KIAA0864 protein	17p11. 2
387 35_ at	Cluster Incl. AB011085:Homo sapiens mRNA for KIAA0513 protein, complete cds /cds=(631,1866) /gb=AB011085 /gi=3043549 /ug=Hs.85053 /len=7758	KIAA0 513	KIAA0513 gene product	16q24. 1

387 47_ at	Cluster Incl. M81945:Human CD34 gene, promoter and /cds=(258,1415) /gb=M81945 /gi=409018 /ug=Hs.85289 /len=2616			
387 67_ at	Cluster Incl. AF041037:Homo sapiens novel antagonist of FGF signaling (sprouty-1) mRNA, partial cds /cds=(0,419) /gb=AF041037 /gi=2827283 /ug=Hs.88044 /len=1586	SPRY 1	sprouty (Drosophila) homolog 1 (antagonist of FGF signaling)	4
387 80_ at	Cluster Incl. J04794:Human aldehyde reductase mRNA, complete cds /cds=(60,1037) /gb=J04794 /gi=178480 /ug=Hs.89529 /len=1132	AKR1 A1	aldo-keto reductase family 1, member A1 (aldehyde reductase)	1p33-p32
387 91_ at	Cluster Incl. D29643:Human mRNA for KIAA0115 gene, complete cds /cds=(106,1476) /gb=D29643 /gi=473936 /ug=Hs.89674 /len=1668	DDOS T	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	1p36.1
388 08_ at	Cluster Incl. D64154:Human mRNA for Mr 110,000 antigen, complete cds /cds=(46,1269) /gb=D64154 /gi=994759 /ug=Hs.90107 /len=1375	GP110	cell membrane glycoprotein, 110000M(r) (surface antigen)	20q13.33
388 12_ at	Cluster Incl. X79683:H.sapiens LAMB2 mRNA for beta2 laminin /cds=(165,5561) /gb=X79683 /gi=663206 /ug=Hs.90291 /len=5673	LAMB 2	laminin, beta 2 (laminin S)	3p21
388	Cluster Incl. AF039103:Homo sapiens	HTATI	HIV-1 Tat	11p15.

24_ at	Tat-interacting protein TIP30 mRNA, complete cds /cds=(12,740) /gb=AF039103 /gi=3043926 /ug=Hs.90753 /len=1297	P2	interactive protein 2, 30 kDa	1
388 33_ at	Cluster Incl. X00457:Human mRNA for SB classII histocompatibility antigen alpha-chain /cds=(0,702) /gb=X00457 /gi=36405 /ug=Hs.914 /len=1048	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	6p21.3
388 58_ at	Cluster Incl. U04270:Human putative potassium channel subunit (h-erg) mRNA, complete cds /cds=(183,3662) /gb=U04270 /gi=487737 /ug=Hs.188021 /len=4070	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	7q35-q36
388 79_ at	Cluster Incl. D83664:Human mRNA for CAAF1 (calcium-binding protein in amniotic fluid 1), complete cds /cds=(68,346) /gb=D83664 /gi=1502286 /ug=Hs.19413 /len=466	S100A12	S100 'calcium-binding protein A12 (calgranulin C)	1q21
388 93_ at	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gi=3136			
388 94_ g_a	Cluster Incl. AL008637:Human DNA sequence from clone 833B7 on chromosome 22q12.3-13.2 Contains			

t	genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS /cds=(629,1648) /gb=AL008637 /gi=3136			
388 95_i _at	Cluster Incl. X77094:H.sapiens mRNA for p40phox /cds=(130,1149) /gb=X77094 /gi=458543 /ug=Hs.196352 /len=1245	NCF4	neutrophil cytosolic factor 4 (40kD)	22q13.1
389 17_ at	Cluster Incl. X73617:H.sapiens mRNA for T-cell receptor delta /cds=UNKNOWN /gb=X73617 /gi=402624 /ug=Hs.2014 /len=2343			
389 49_ at	Cluster Incl. L01087:Human protein kinase C-theta (PRKCT) mRNA, complete cds /cds=(94,2214) /gb=L01087 /gi=558098 /ug=Hs.211593 /len=2754	PRKC Q	protein kinase C, theta	10p15
389 63_i _at	Cluster Incl. U12707:Human Wiskott-Aldrich syndrome protein (WASP) mRNA, complete cds /cds=(34,1542) /gb=U12707 /gi=695150 /ug=Hs.2157 /len=1806	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	Xp11.4 - p11.21
389 92_ at	Cluster Incl. X64229:H.sapiens dek mRNA /cds=(33,1160) /gb=X64229 /gi=30502 /ug=Hs.110713 /len=2699	DEK	DEK oncogene (DNA binding)	6p23
389 94_ at	Cluster Incl. AF037989:Homo sapiens STAT-induced STAT inhibitor-2 mRNA, complete cds /cds=(317,913)	STAT1 2	STAT induced STAT inhibitor-2	12q

at	/gb=AF037989 /gi=3265032 /ug=Hs.110776 /len=1937			
390 61_ at	Cluster Incl. D28137:Human mRNA for BST-2, complete cds /cds=(9,551) /gb=D28137 /gi=457563 /ug=Hs.118110 /len=996	BST2	bone marrow stromal cell antigen 2	19p13. 2
390 62_ at	Cluster Incl. AL008726:dJ337O18.2 (Lysosomal Protective Protein precursor (EC 3.4.16.5, Cathepsin A, Carboxypeptidase C)) /cds=(133,1575) /gb=AL008726 /gi=3183870 /ug=Hs.118126 /len=1946			
390 70_ at	Cluster Incl. U03057:Human actin bundling protein (HSN) mRNA, complete cds /cds=(111,1592) /gb=U03057 /gi=458027 /ug=Hs.118400 /len=2767	SNL	singed (Drosophila)-like (sea urchin fascin homolog like)	7p22
390 89_ at	Cluster Incl. Y07604:H.sapiens mRNA for nucleoside-diphosphate kinase /cds=(11,574) /gb=Y07604 /gi=1945761 /ug=Hs.9235 /len=879	NME4	non-metastatic cells 4, protein expressed in	16p13. 3
391 18_ at	Cluster Incl. L08069:Human heat shock protein, E. coli DnaJ homologue mRNA, complete cds /cds=(82,1275) /gb=L08069 /gi=306713 /ug=Hs.94 /len=1438	DNAJ A1	DnaJ (Hsp40) homolog, subfamily A, member 1	9p13- p12
391 36_ at	Cluster Incl. AB017642:Homo sapiens mRNA for oxidative-stress responsive 1, complete cds /cds=(342,1925) /gb=AB017642 /gi=4519628	OSR1	oxidative-stress responsive 1	3p22- p21.3

	/ug=Hs.95220 /len=4519			
391 65_ at	Cluster Incl. U47101:Human NifU-like protein (hNifU) mRNA, partial cds /cds=(0,366) /gb=U47101 /gi=1685101 /ug=Hs.9908 /len=819	NIFU	nitrogen fixation cluster-like	12q24.1
391 70_ at	"Cluster Incl. AL049957:Homo sapiens mRNA; cDNA DKFZp564J0323 (from clone DKFZp564J0323) /cds=UNKNOWN /gb=AL049957 /gi=4884209 /ug=Hs.99766 /len=2180"			
391 79_ at	Cluster Incl. Z26248:H.sapiens mRNA for eosinophil granule major basic protein /cds=(857,1525) /gb=Z26248 /gi=940510 /ug=Hs.99962 /len=1637	PRG2	proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)	11q12
392 62_ at	Cluster Incl. U79266:Human clone 23627 mRNA, complete cds /cds=(184,1041) /gb=U79266 /gi=1710225 /ug=Hs.23642 /len=1561	HSU79 266	protein predicted by clone 23627	11q13.1
393 01_ at	Cluster Incl. X85030:H.sapiens mRNA for skeletal muscle-specific calpain /cds=(0,2465) /gb=X85030 /gi=791039 /ug=Hs.239689 /len=2466	CAPN 3	calpain 3, (p94)	15q15.1-q21.1
393 27_ at	Cluster Incl. D86983:Human mRNA for KIAA0230 gene, partial cds /cds=(0,4490) /gb=D86983 /gi=1504039 /ug=Hs.118893 /len=5510	D2S44 8	Melanoma associated gene	2pter-p25.1

393 58_ at	Cluster Incl. U37146:Human silencing mediator of retinoid and thyroid hormone action (SMRT) mRNA, complete cds /cds=(495,4982) /gb=U37146 /gi=1045654 /ug=Hs.120980 /len=5970			
396 10_ at	Cluster Incl. X16665:Human HOXB2 mRNA from the Hox2 locus /cds=(78,1148) /gb=X16665 /gi=32381 /ug=Hs.2733 /len=1520	HOXB 2	homeo box B2	17q21- q22
396 49_ at	Cluster Incl. X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817 /gi=840785 /ug=Hs.3109 /len=3236	ARHG AP4	Rho GTPase activating protein 4	Xq28
396 70_ at	"Cluster Incl. AL050034:Homo sapiens mRNA; cDNA DKFZp566G0224 (from clone DKFZp566G0224) /cds=(0,1380) /gb=AL050034 /gi=4884274 /ug=Hs.33573 /len=1762"	ADPR TL3	"ADP- ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 3"	3p22.2 -p21.1
396 89_ at	Cluster Incl. AI362017:qy39a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2014362 /clone_end=3 /gb=AI362017 /gi=4113638 /ug=Hs.135084 /len=778	CST3	cystatin C (amyloid angiopathy and cerebral hemorrhage)	20p11. 2
397 30_ at	Cluster Incl. X16416:Human c-abl mRNA encoding p150 protein /cds=(147,3539) /gb=X16416 /gi=28236 /ug=Hs.146355 /len=5527	ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	9q34.1
397 55_ at	Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on			

at	chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802			
397 56_ g_a t	Cluster Incl. Z93930:Human DNA sequence from clone 292E10 on chromosome 22q11-12. Contains the XBP1 gene for X-box binding protein 1 (TREB5), ESTs, STSs, GSSs and a putative CpG island /cds=(30,815) /gb=Z93930 /gi=4775603 /ug=Hs.149923 /len=1802			
397 75_ at	Cluster Incl. X54486:Human gene for C1-inhibitor /cds=(60,1562) /gb=X54486 /gi=29534 /ug=Hs.151242 /len=1827			
398 01_ at	Cluster Incl. AF046889:Homo sapiens lysyl hydroxylase isoform 3 (PLOD3) mRNA, complete cds /cds=(216,2432) /gb=AF046889 /gi=3153234 /ug=Hs.153357 /len=2735	PLOD 3	procollagen- lysine, 2- oxoglutarate 5- dioxygenase 3	7q22
398 14_ s_at	Cluster Incl. AI052724:oz27a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1676542 /clone_end=3 /gb=AI052724 /gi=3308715 /ug=Hs.109201 /len=682	LOC51 635	CGI-86 protein	14q23. 1
398 24_ at	Cluster Incl. AI391564:tg16b02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2108907 /clone_end=3		ESTs, Weakly similar to A28996 proline-	

at	/gb=AI391564 /gi=4217568 /ug=Hs.110820 /len=442		rich protein M14 precursor mouse [M.musculus]	
398 27_ at	Cluster Incl. AA522530:ni38d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-979127 /clone_end=3 /gb=AA522530 /gi=2263242 /ug=Hs.111244 /len=891	FLJ20 500	hypothetical protein	10pter- q26.12
398 60_ at	Cluster Incl. U05040:Human FUSE binding protein mRNA, complete cds /cds=(26,1960) /gb=U05040 /gi=460151 /ug=Hs.118962 /len=2325		Homo sapiens far upstream element (FUSE) binding protein 1 (FUBP1), mRNA	
399 21_ at	Cluster Incl. AI526089:DU3.2-7.H07.r Homo sapiens cDNA, 5 end /clone_end=5 /gb=AI526089 /gi=4440207 /ug=Hs.1342 /len=788	COX5 B	cytochrome c oxidase subunit Vb	2cen- q13
399 29_ at	Cluster Incl. AB023139:Homo sapiens mRNA for KIAA0922 protein, partial cds /cds=(0,2372) /gb=AB023139 /gi=4589475 /ug=Hs.37892 /len=2505	KIAA0 922	KIAA0922 protein	4q31.3
399 68_ at	Cluster Incl. U50136:Human leukotriene C4 synthase (LTC4S) gene, complete cds /cds=(96,548) /gb=U50136 /gi=1314482 /ug=Hs.456 /len=665			
399 93_ at	Cluster Incl. D11466:Homo sapiens mRNA for PIG-A protein, complete cds	PIGA	phosphatidylinositol glycan,	Xp22.1

at	/cds=(85,1539) /gb=D11466 /gi=219993 /ug=Hs.51 /len=3589		class A (paroxysmal nocturnal hemoglobinuria)	
400 81_ at	Cluster Incl. L26232:Human phospholipid transfer protein mRNA, complete cds /cds=(87,1568) /gb=L26232 /gi=468325 /ug=Hs.154854 /len=1750	PLTP	phospholipid transfer protein	20q12- q13.1
401 59_ r_at	Cluster Incl. M55067:Human 47-kD autosomal chronic granulomatous disease protein mRNA, complete cds /cds=(22,1194) /gb=M55067 /gi=189050 /ug=Hs.1583 /len=1349	NCF1	neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1)	7q11.2 3
401 98_ at	Cluster Incl. L06132:Human voltage- dependent anion channel isoform 1 (VDAC) mRNA, complete cds /cds=(99,950) /gb=L06132 /gi=340198 /ug=Hs.149155 /len=1806	VDAC 1	voltage- dependent anion channel 1	5q31
402 81_ at	Cluster Incl. D63878:Human mRNA for KIAA0158 gene, complete cds /cds=(258,1343) /gb=D63878 /gi=961447 /ug=Hs.155595 /len=3433	NEDD 5	neural precursor cell expressed, developmentally down-regulated 5	2q37
402 82_ s_at	Cluster Incl. M84526:Human adipsin/complement factor D mRNA, complete cds /cds=(54,740) /gb=M84526 /gi=178625 /ug=Hs.155597 /len=1071	DF	D component of complement (adipsin)	19p13. 3

403 96_ at	Cluster Incl. U49395:Human ionotropic ATP receptor P2X5a mRNA, complete cds /cds=(52,1317) /gb=U49395 /gi=1552521 /ug=Hs.77807 /len=1956	P2RX5	purinergic receptor P2X, ligand-gated ion channel, 5	17p13
404 07_ at	Cluster Incl. U28386:Human nuclear localization sequence receptor hSRP1alpha mRNA, complete cds /cds=(132,1721) /gb=U28386 /gi=899538 /ug=Hs.159557 /len=1976	KPNA 2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	17q23.1-q23.3
404 19_ at	Cluster Incl. X85116:H.sapiens epb72 gene exon 1 /cds=(61,927) /gb=X85116 /gi=1161561 /ug=Hs.160483 /len=3035			
404 56_ at	"Cluster Incl. AL049963:Homo sapiens mRNA; cDNA DKFZp564A132 (from clone DKFZp564A132) /cds=UNKNOWN /gb=AL049963 /gi=4884213 /ug=Hs.16726 /len=1322"			
404 93_ at	Cluster Incl. L05424:Human hyaluronate receptor (CD44) gene /cds=(136,2211) /gb=L05424 /gi=950415 /ug=Hs.169610 /len=2905			
405 09_ at	Cluster Incl. J04058:Human electron transfer flavoprotein alpha-subunit mRNA, complete cds /cds=(0,1001) /gb=J04058 /gi=182250 /ug=Hs.169919 /len=1266	ETFA	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	15q23-q25
405	Cluster Incl. D25538:Human mRNA for	ADCY	adenylate	16q12-

85_ at	KIAA0037 gene, complete cds /cds=(265,3507) /gb=D25538 /gi=436217 /ug=Hs.172199 /len=6196	7	cyclase 7	q13
406 10_ at	Cluster Incl. AI743507:wf72a06.x2 Homo sapiens cDNA, 3 end /clone=IMAGE-2361106 /clone_end=3 /gb=AI743507 /gi=5111795 /ug=Hs.173518 /len=733	ZFR	zinc finger RNA binding protein	5p13.3
406 98_ at	Cluster Incl. X96719:H.sapiens mRNA for AICL (activation-induced C-type lectin) /cds=(132,581) /gb=X96719 /gi=1632815 /ug=Hs.85201 /len=739	CLEC SF2	C-type (calcium dependent, carbohydrate- recognition domain) lectin, superfamily member 2 (activation- induced)	12p13- p12
407 18_ at	Cluster Incl. AF013611:Homo sapiens lymphopain mRNA, complete cds /cds=(0,1130) /gb=AF013611 /gi=2582044 /ug=Hs.87450 /len=1131	CTSW	cathepsin W (lymphopain)	11q13. 1
407 23_ at	Cluster Incl. AJ010059:Homo sapiens SIT protein /cds=(87,677) /gb=AJ010059 /gi=4688891 /ug=Hs.88012 /len=1232	SIT	SHP2 interacting transmembrane adaptor	9p13- p12
407 63_ at	Cluster Incl. U85707:Human leukemogenic homolog protein (MEIS1) mRNA, complete cds /cds=(65,1237) /gb=U85707 /gi=2058550 /ug=Hs.170177 /len=2511	MEIS1	Meis1 (mouse) homolog	2p14- p13

407 67_ at	Cluster Incl. M59499:Human lipoprotein-associated coagulation inhibitor (LACI) gene /cds=(2,916) /gb=M59499 /gi=187205 /ug=Hs.170279 /len=3599			
407 75_ at	Cluster Incl. AL021786:Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs /cds=(0,680) /gb=AL021786 /gi=2853186 /ug=Hs.17109 /len=1389			
407 86_ at	Cluster Incl. U37352:Human protein phosphatase 2A Balphal regulatory subunit mRNA, complete cds /cds=(88,1632) /gb=U37352 /gi=1203811 /ug=Hs.171734 /len=4064	PPP2 R5C	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	3p21
408 17_ at	Cluster Incl. M96824:Human nucleobindin precursor mRNA, complete cds /cds=(39,1421) /gb=M96824 /gi=189307 /ug=Hs.172609 /len=1650	NUCB 1	nucleobindin 1	19q13.2-q13.4
408 56_ at	Cluster Incl. U29953:Human pigment epithelium-derived factor gene, complete cds /cds=(136,1224) /gb=U29953 /gi=1144298 /ug=Hs.173594 /len=1511			
408 64_ at	Cluster Incl. D25274:Homo sapiens mRNA, clone-PO2ST9 /cds=UNKNOWN /gb=D25274 /gi=464185 /ug=Hs.173737 /len=1232			

	/gi=464185 /ug=Hs.173737 /len=1232			
408 65_ at	Cluster Incl. U51166:Human G/T mismatch-specific thymine DNA glycosylase mRNA, complete cds /cds=(399,1631) /gb=U51166 /gi=1378106 /ug=Hs.173824 /len=3410	TDG	thymine-DNA glycosylase	12q24.1
409 36_ at	Cluster Incl. AI651806:wb55f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2309611 /clone_end=3 /gb=AI651806 /gi=4735797 /ug=Hs.19280 /len=609	CRIM1	cysteine-rich motor neuron 1	2p21
410 96_ at	Cluster Incl. AI126134:qd77c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1735496 /clone_end=3 /gb=AI126134 /gi=3594648 /ug=Hs.100000 /len=446	S100A8	S100 calcium-binding protein A8 (calgranulin A)	1q21
411 38_ at	Cluster Incl. M16279:Human MIC2 mRNA, complete cds /cds=(177,734) /gb=M16279 /gi=188542 /ug=Hs.177543 /len=1238	MIC2	antigen identified by monoclonal antibodies 12E7, F21 and O13	Xp22.32
411 53_ f_at	Cluster Incl. AF102803:untitled /cds=(2,2722) /gb=AF102803 /gi=4092760 /ug=Hs.178452 /len=3668			
411 55_ at	Cluster Incl. U03100:Human alpha2(E)-catenin mRNA, complete cds /cds=(4,2799) /gb=U03100 /gi=414981 /ug=Hs.178452 /len=3526	CTNN A1	catenin (cadherin-associated protein), alpha 1 (102kD)	5q31

			(102kD)	
411 56_ g_a t	Cluster Incl. U03100:Human alpha2(E)-catenin mRNA, complete cds /cds=(4,2799) /gb=U03100 /gi=414981 /ug=Hs.178452 /len=3526	CTNN A1	catenin (cadherin- associated protein), alpha 1 (102kD)	5q31
411 63_ at	Cluster Incl. AL109672:Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 755868 /cds=(98,751) /gb=AL109672 /gi=5689836 /ug=Hs.179516 /len=1378	P24B	integral type I protein	15q24- q25
411 64_ at	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	IGHM	immunoglobulin heavy constant mu	14q32. 33
411 65_ g_a t	Cluster Incl. X67301:H.sapiens mRNA for IgM heavy chain constant region (Ab63) /cds=(0,1361) /gb=X67301 /gi=38407 /ug=Hs.179543 /len=1453	IGHM	immunoglobulin heavy constant mu	14q32. 33
411 66_ at	Cluster Incl. X58529:Human rearranged immunoglobulin mRNA for mu heavy chain enhancer and constant region /cds=UNKNOWN /gb=X58529 /gi=33480 /ug=Hs.179543 /len=2325			
411 77_ at	Cluster Incl. AW024285:wt69d06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2512715 /clone_end=3 /gb=AW024285 /gi=5877815	FLJ12 443	hypothetical protein FLJ12443	5p15.3 3

	/ug=Hs.179882 /len=550			
411 91_ at	Cluster Incl. AB023209:Homo sapiens mRNA for KIAA0992 protein, partial cds /cds=(0,2318) /gb=AB023209 /gi=4589627 /ug=Hs.180347 /len=4347	KIAA0992	palladin	4q32.3
411 93_ at	Cluster Incl. AB013382:Homo sapiens mRNA for DUSP6, complete cds /cds=(351,1496) /gb=AB013382 /gi=3869139 /ug=Hs.180383 /len=2390	DUSP6	dual specificity phosphatase 6	12q22-q23
412 00_ at	Cluster Incl. Z22555:H.sapiens encoding CLA-1 mRNA /cds=(69,1598) /gb=Z22555 /gi=397606 /ug=Hs.180616 /len=2552	CD36L1	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1	12q24.31
412 20_ at	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938	MSF	MLL septin-like fusion	17q25
412 73_ at	Cluster Incl. AL046940:DKFZp586I0517_r1 Homo sapiens cDNA, 5 end /clone=DKFZp586I0517 /clone_end=5 /gb=AL046940 /gi=5434999 /ug=Hs.231657 /len=695			
413 38_ at	Cluster Incl. AI951946:wx39f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2546059 /clone_end=3 /gb=AI951946 /gi=5744256 /ug=Hs.244 /len=523			

413 96_ at	Cluster Incl. AB006629:Homo sapiens mRNA for KIAA0291 gene, partial cds /cds=(0,2856) /gb=AB006629 /gi=2564329 /ug=Hs.104717 /len=4943	CYLN2	cytoplasmic linker 2	7q11.2 3
414 70_ at	Cluster Incl. AF027208:Homo sapiens AC133 antigen mRNA, complete cds /cds=(37,2634) /gb=AF027208 /gi=2688948 /ug=Hs.112360 /len=3794	PROM L1	prominin (mouse)-like 1	4p15.3 3
414 71_ at	Cluster Incl. W72424:zd66a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345592 /clone_end=3 /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604	S100A 9	S100 calcium-binding protein A9 (calgranulin B)	1q21
415 03_ at	Cluster Incl. AB020661:Homo sapiens mRNA for KIAA0854 protein, complete cds /cds=(304,2817) /gb=AB020661 /gi=4240196 /ug=Hs.30209 /len=4089	KIAA0 854	KIAA0854 protein	8q24.1 3
415 35_ at	Cluster Incl. AF006484:Homo sapiens putative oral tumor suppressor protein (doc-1) mRNA, complete cds /cds=(522,869) /gb=AF006484 /gi=2738496 /ug=Hs.3436 /len=1608	CDK2 AP1	CDK2-associated protein 1	12q24. 31
415 47_ at	Cluster Incl. AF047472:Homo sapiens spleen mitotic checkpoint BUB3 (BUB3) mRNA, complete cds /cds=(70,1056) /gb=AF047472 /gi=2921872 /ug=Hs.40323 /len=2585	BUB3	BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog	10q26
416 09_ at	Cluster Incl. U15085:Human HLA-DMB mRNA, complete cds /cds=(233,1024) /gb=U15085 /gi=557701 /ug=Hs.1162	HLA- DMB	major histocompatibility complex, class	6p21.3

at	/len=1362		II, DM beta	
416 54_ at	Cluster Incl. X02994:Human mRNA for adenosine deaminase (adenosine aminohydrolase, EC 3.5.4.4) /cds=(95,1186) /gb=X02994 /gi=28379 /ug=Hs.1217 /len=1498	ADA	adenosine deaminase	20q12-q13.11
416 60_ at	Cluster Incl. AL031588:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar to rat MEG /cds=(0,4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438	GTSE 1	G-2 and S-phase expressed 1	22q13.2-q13.3
416 94_ at	Cluster Incl. M17754:Human BN51 mRNA, complete cds /cds=(51,1238) /gb=M17754 /gi=179512 /ug=Hs.1276 /len=1881	BN51T	BN51 (BHK21) temperature sensitivity complementing	8q21
417 23_ s_at	Cluster Incl. M32578:Human MHC class II HLA-DR beta-1 mRNA (DR2.3), 5end /cds=(61,861) /gb=M32578 /gi=188305 /ug=Hs.181366 /len=1216	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	6p21.3
417 34_ at	Cluster Incl. AB020677:Homo sapiens mRNA for KIAA0870 protein, complete cds /cds=(436,1998) /gb=AB020677 /gi=4240228 /ug=Hs.18166 /len=4484	KIAA0870	KIAA0870 protein	8q24.3
417 47_ s_at	Cluster Incl. U49020:Human myocyte-specific enhancer factor 2A (MEF2A) gene, first coding /cds=(142,1662) /gb=U49020 /gi=1197536			

	/ug=Hs.182280 /len=5329			
417 63_ g_a t	Cluster Incl. D64015:Homo sapiens mRNA for T-cluster binding protein, complete cds /cds=(157,954) /gb=D64015 /gi=2281005 /ug=Hs.182741 /len=1737	TIAL1	TIA1 cytotoxic granule-associated RNA-binding protein-like 1	10q
417 96_ at	Cluster Incl. AB029015:Homo sapiens mRNA for KIAA1092 protein, partial cds /cds=(0,3464) /gb=AB029015 /gi=5689520 /ug=Hs.54886 /len=4147	PLCE2	phospholipase C, epsilon 2	3p24.3
418 08_ at	Cluster Incl. AF052102:Homo sapiens clone 23926 mRNA sequence /cds=UNKNOWN /gb=AF052102 /gi=3360409 /ug=Hs.5671 /len=1884			
418 09_ at	Cluster Incl. AI656421:tt50h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2244259 /clone_end=3 /gb=AI656421 /gi=4740400 /ug=Hs.5671 /len=566	MGC4 175	hypothetical protein MGC4175	7q21.1 -q21.2
418 47_ at	Cluster Incl. AA214546:zr92c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-683140 /clone_end=3 /gb=AA214546 /gi=1813171 /ug=Hs.66576 /len=516	IL24	interleukin 24	1q32
432 _s_ at	X02883 /FEATURE=cds /DEFINITION=HSTCRAC Human gene for T-cell receptor alpha chain C region	TRA	T cell receptor alpha locus	14q11.2
484 _at	U59302 /FEATURE= /DEFINITION=HSU59302 Human	NCOA 1	nuclear receptor coactivator 1	2p23

_at	steroid receptor coactivator-1 F-SRC-1 mRNA, complete cds	1	coactivator 1	
529 _at	U15932 /FEATURE= /DEFINITION=HSU15932 Human dual-specificity protein phosphatase mRNA, complete cds	DUSP 5	dual specificity phosphatase 5	10q25
538 _at	S53911 /FEATURE= /DEFINITION=S53911 CD34=glycoprotein expressed in lymphohematopoietic progenitor cells {alternatively spliced, truncated form} [human, UT7, mRNA, 2657 nt]	CD34	CD34 antigen	1q32
585 _at	M30938 /FEATURE=mRNA#2 /DEFINITION=HUMKUP Human Ku (p70/p80) subunit mRNA, complete cds	XRCC 5	"X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand- break rejoining; Ku autoantigen, 80kD)"	2q35
605 _at	L78833 /FEATURE=exon#36 /DEFINITION=HUMBRCA1 Human BRCA1, Rho7 and vat1 genes, complete cds, and ipf35 gene, partial cds			
706 _at	Glucocorticoid Receptor, Beta			
767 _at	AF001548 /FEATURE=mRNA /DEFINITION=HUA001548 Human			

_at	Chromosome 16 BAC clone CIT987SK-A-815A9, sequence complete			
820 _at	U77604 /FEATURE= /DEFINITION=HSU77604 Homo sapiens microsomal glutathione S- transferase 2 (MGST2) mRNA, complete cds	MGST 2	microsomal glutathione S- transferase 2	4q28- q31
854 _at	S76617 /FEATURE= /DEFINITION=S76617 blk=protein tyrosine kinase [human, B lymphocytes, mRNA, 2608 nt]	BLK	B lymphoid tyrosine kinase	8p23- p22
931 _at	L08177 /FEATURE= /DEFINITION=HUMGPCRB Human EBV induced G-protein coupled receptor (EBI2) mRNA, complete cds	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte- specific G protein-coupled receptor)	13q32. 3
932 _i_a t	L11672 /FEATURE= /DEFINITION=HUMKRUPZN Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds	ZNF91	zinc finger protein 91 (HPF7, HTF10)	19p13. 1-p12
933 _f_ at	L11672 /FEATURE= /DEFINITION=HUMKRUPZN Human Kruppel related zinc finger protein (HTF10) mRNA, complete cds	ZNF91	zinc finger protein 91 (HPF7, HTF10)	19p13. 1-p12
958 _s_	Rna Polymerase II, 14.5 Kda Subunit			

at				
AFF X- HU MR GE/ M1 009 8_ M_ at	M10098 Human 18S rRNA gene, complete (_5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)			

Table 22:

Pairwise Comparisons

<i>Classification</i>		nBM	CLL	CML	ALL	AML	
	nBM		KIA0952, BNI	IRF4, HLA-DMB	PLSCR1, KCN2 KIAA0482*	PLSCR1, CAMP	n=8
	CLL	100% (1.00)		TBB, HLA-DMB	NOCA1, US2981*	POU2AF1, TNFR857	n=8
	CML	100% (1.00)	100% (1.00)		CLC, TALDD1	DEFA3, LCN2, SOP28*	n=10
	ALL	100% (0.97)	100% (1.00)	100% (1.00)		OS-8*, LEF1, MSF, PP08, APLE2	n=18
	AML	100% (1.00)	100% (1.00)	100% (0.96)	97% (0.95)		n=59
		n=8	n=8	n=10	n=18	n=59	
	% = accuracy in leave-one-out cross validation.						
	() = confidence.						

Table 23:

Golub				diffgenes			
A - Samples: 18 / 85				A - samples: 18 / 85			
Accuracy 0,87				accuracy 0,96			
Confidence 0,77				confidence 0,88			
Failed 6,19,22,26,78,79,80,81,82,83,84,85,99				failed 5,6,19,22			
Gene	Signal-to-noise	p	decision limit	gene	signal-to-noise	p	decision limit
g1	-1,14	0*	482,01	g1	-1,14	0	
g2	-1,06	0*	192,17	g2	-1,06	0*98,50	
g3	-0,97	0*	207,67	g3	-0,97	0	
g4	0,94	0*	205,05	g4	0,94	0	
g5	-0,93	0*	1818,11	g5	-0,93	0	
g6	0,93	0*	451,74	g6	0,93	0	
g7	-0,91	0*	23,84	g7	-0,91	0	
g8	-0,90	0*	225,72	g8	-0,90	0	

g9	0,90	0*	43,85	g9	0,90	0	
g10	0,89	0*	210,78	g10	0,89	0	
g11	-0,88	0*	118,63	g11	-0,88	0	
g12	0,87	0*	55,39	g12	0,87	0*	67,80
g13	0,87	0*	127,15	g13	0,87	0*	164,10
g14	0,86	0*	222,04	g14	0,86	0	
g15	0,85	0*	68,52	g15	0,85	0	
g16	-0,85	0*	546,97	g16	-0,85	0	
g17	0,84	0*	1242,77	g17	0,84	0	
g18	-0,84	0*	162,61	g18	-0,84	0	
g19	-0,83	0*	385,39	g19	-0,83	0	
g20	0,46	0*	105,38	g20	0,46	0	

Table 24:

Classes	t(15;17) vs. t(8;21)	t(15;17) vs. inv(16)	inv(16) vs. t(8;21)	inv(16) vs. remainder	t(8;21) vs. remainder	t(15;17) vs. remainder
Accuracy	1.00	1.00	1.00	1.00	1.00	1.00
Prediction strength	0.91	0.96	0.93	0.95	0.98	0.91
M65066				-1.52		
AL049933						-2.12
AF010310						1.89
N90866						-2.34
M26326	2.85				-2.56	

N99340				8.43			
M25915							1.63
P(g,c) AF013570			-6.84	7.78	6.99		
			3.08				3.08
AI207842	3.08						
X16665				6.56	6.56		
X96719							-2.36
AF013611	2.68						
W72424							-2.05

Table 25

GenBank accession No.	Approved UCL/HGNC/HUGO database symbol	Description	Identified according to Golub et al.	Identified utilizing multiple-tree classifiers
M65066	<i>PRKAR1B</i>	cAMP-dependent protein kinase regulatory subunit RI-beta	X	
AL049933	<i>GNAI1</i>	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1	X	
AF010310	<i>PIG6*</i>	proline oxidase homolog	X	
N90866	<i>CDW52</i>	CDW52 antigen (CAMPATH-1 antigen)	X	
M26326	<i>KRT18</i>	keratin, type I cytoskeletal 18	X	X
N99340	<i>DKFZP586N1922</i> *	DKFZP586N1922 protein	X	X
M25915	<i>CLU</i>	clusterin precursor	X	
A1207842	<i>PTGDS</i>	prostaglandin-h2 d-isomerase precursor	X	
X16665	<i>HOXB2</i>	homeobox protein hox-b2	X	X
X96719	<i>CLECSF2</i>	C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 2 (activation-induced)	X	X
AF013611	<i>CTSW</i>	cathepsin w (lymphopain) precursor	X	X
W72424	<i>S100A9</i>	calgranulin b (migration inhibitory factor-related protein 14)	X	
AF013570	<i>MYH11</i>	myosin heavy chain, smooth muscle isoform	X	X
AF001548	<i>MYH11</i>	myosin heavy chain, smooth muscle isoform		X

X53742	<i>FBLN1</i>	fibulin-1		X
U37122	<i>ADD3</i>	gamma adducin		X
J03853	<i>ADRA2C</i>	alpha-2c-1 adrenergic receptor		X
Y10183	<i>ALCAM</i>	CD166 antigen precursor (activated leukocyte-cell adhesion molecule)		X
AB002313	<i>PLXNB2</i>	plexin B2		X
X78817	<i>ARHGAP4</i>	rho GTPase activating protein 4		X
X54486	<i>SERPING1</i>	plasma protease c1 inhibitor precursor		X
L19872	<i>AHR</i>	aryl hydrocarbon receptor		X
M15395	<i>ITGB2</i>	CD18, integrin beta-2 precursor		X
AF045229	<i>RGS10</i>	regulator of g-protein signaling 10		X
D43638	<i>CBFA2T1</i>	MTG8 protein (ETO protein)		X
M25280	<i>SELL</i>	L-selectin precursor (lymph node homing receptor)		X
W25986	<i>DKFZP564K0822</i> *	hypothetical protein DKFZp564K0822		X
M36035	<i>BZRP</i>	peripheral-type benzodiazepine receptor		X
X64624	<i>POU4F1</i>	brain-specific homeobox/pou domain protein 3a		X
M18728	<i>CEACAM6</i>	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)		X
M77349	<i>TGFB1</i>	transforming growth factor-beta induced protein ig-h3 precursor		X

M80899	AHNAK	neuroblast differentiation associated protein ahnak		X
M13560	CD74	CD74 antigen, (invariant polypeptide of major histocompatibility complex, class II antigen-associated)		X
X62744	HLA-DMA	major histocompatibility complex, class II, DM alpha, RING6		X
M32578	HLA-DRB1	HLA class II histocompatibility antigen, dr-1(dw14) beta chain precursor		X
X00457	HLA-DPA1	HLA class II histocompatibility antigen, dp alpha chain precursor		X
J00194	HLA-DRA	HLA class II histocompatibility antigen, dr alpha chain precursor		X

Table 26: Comparisons of protein expression and mRNA abundance in acute myeloid leukemia as assessed by flow cytometry and microarray analysis

Antigen	Number of comparisons	Both FC and MA positive	Both FC and MA negative	MA positive and FC negative	FC positive and MA negative
Myeloperoxidase	25	25	-	-	-
CD13	25	24	-	-	1
CD33	25	24	-	-	1
CD45	21	21	-	-	-
HLA-DR	10	10	-	-	-
CD135	4	3	-	1	-
CD61	19	-	19	-	-
CD10	15	-	15	-	-
CD235a	14	-	12	2	-
NG2	11	-	11	-	-
CD22	5	-	5	-	-
CD133	4	-	4	-	-
CD79a	2	-	1	1	-
CD14	23	6	14	3	-
CD34	22	17	4	1	-
CD2	22	16	3	3	-
CD7	22	14	8	-	-
CD15	19	15	1	3	-
CD3	9	4	4	1	-
Lactoferrin	13	8	2	3	-
CD116	6	4	2	-	-
CD11b	7	5	2	-	-
CD19	12	5	2	5	-
CD36	22	2	14	-	6
CD38	9	4	1	-	4
CD4	18	6	7	2	3
CD56	23	2	17	-	4
CD64	23	15	4	3	1
TdT	20	-	17	2	1
Total	450 (100%)	230 (51.1%)	169 (37.6%)	30 (6.7%)	21 (4.7%)
		399 (88.7%) congruent		51 (11.4%) not congruent	

Protein expression and mRNA abundance were compared in 25 patients. "Number of 5 comparisons" indicates the number of patients analyzed for the respective antigens (maximum number, 25 patients)

Table 27

Affymetrix_ID	Description_microarray	Symbol	Description_NetAffx	Chromosome
1087_at	M60459 /FEATURE= /DEFINITION=HUMERYTH Human erythropoietin receptor mRNA, complete cds	EPOR	erythropoietin receptor	19p13.3-p13.2
1747_at	AD000092 /FEATURE=cds#2 /DEFINITION=CH19HHR23 Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence	unknown cDNA*	?	
1752_at	AD000092 /FEATURE=cds#6 /DEFINITION=CH19HHR23 Homo sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence	unknown cDNA*	?	
180_at	S82470 /FEATURE= /DEFINITION=S82470 BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]	LENG4	leukocyte receptor cluster (LRC) member 4	19q13.4
206_at	M84424 /FEATURE=expanded_cds /DEFINITION=HUMCTSE09 Human cathepsin E (CTSE) gene, exon 9 and	CTSE	cathepsin E	

complete cds		
31381_ at	Cluster Incl. AF076483:Homo sapiens peptidoglycan recognition protein precursor (PGRP) mRNA, complete cds /cds=(44,634) /gb=AF076483 /gi=3342532 /ug=Hs.137583 /len=690	PGLYRP peptidoglycan recognition protein 19q13.2- q13.3
31682_ s_at	Cluster Incl. D32039:Human pgH3 mRNA for proteoglycan PG-M(V3), complete cds /cds=(105,2072) /gb=D32039 /gi=1008912 /ug=Hs.234753 /len=2087	CSPG2 chondroitin sulfate proteoglycan 2 (versican) 5q14.3
31749_ f_at	Cluster Incl. Z98744:histone H2A /cds=(7,399) /gb=Z98744 /gi=3080457 /ug=Hs.131954 /len=499	H2AFN H2A histone family, member N 6p22-p21.3
32323_ at	Cluster Incl. M63582:Human preprothyrotropin-releasing hormone gene /cds=(8,736) /gb=M63582 /gi=190297 /ug=Hs.182231 /len=1457	TRH thyrotropin- releasing hormone 3q13.3-q21
33093_ at	Cluster Incl. AF077346:Homo sapiens interleukin-18 receptor accessory protein-like mRNA, complete cds /cds=(483,2282) /gb=AF077346 /gi=3851059 /ug=Hs.158315 /len=2681	IL18RAP interleukin 18 receptor accessory protein 2p24.3- p24.1
33584_ at	Cluster Incl. U35146:Human p56 KKIAMRE protein kinase (KKIAMRE), complete cds /cds=(0,1481) /gb=U35146 /gi=1517819 /ug=Hs.158512 /len=1482	CDKL2 cyclin- dependent kinase-like 2 (CDC2-related kinase) 4
34110_ g_at	Cluster Incl. AF010310:Homo sapiens p53 induced protein mRNA, partial cds /cds=(0,761) /gb=AF010310 /gi=2415296	P1G6 proline oxidase homolog

/ug=Hs.211605 /len=888			
34139_	Cluster Incl. AL049651:Human DNA sequence from clone 753D10 on chromosome 20 Contains genes for SSTR4(somatostatin receptor 4) and at THBD(thrombomodulin), ESTs, STSs, GSSs and CpG islands /cds=(98,1264) /gb=AL049651 /gi=4741619 /ug=Hs.226015 /len=1427	SSTR4	somatostatin receptor 4 20p11.2
34800_	Cluster Incl. AL039458:DKFZp434N0910_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434N0910 /clone_end=3 at /gb=AL039458 /gi=5408506 /ug=Hs.4193 /len=849	LIG1	ortholog of mouse integral membrane glycoprotein LIG-1
34960_	Cluster Incl. M15059:Human Fc-epsilon receptor (IgE receptor) mRNA, complete cds g_at (H107 epitope) /cds=(213,1178) /gb=M15059 /gi=182447 /ug=Hs.1416 /len=1530	FCER2	Fc fragment of IgE, low affinity II, receptor for (CD23A) 19p13.3
35179_	Cluster Incl. AB009598:Homo sapiens mRNA for glucuronyltransferase I, complete cds /cds=(29,1036) /gb=AB009598 at /gi=3892639 /ug=Hs.26492 /len=1441	B3GAT3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I) 11q12.2
35426_	Cluster Incl. AC004410:Homo sapiens chromosome 19, fosmid 39554 at /cds=(0,1196) /gb=AC004410 /gi=2959558 /ug=Hs.167352 /len=1197	LOC56928	hypothetical protein from EUROIMAGE 42353 19p13.3
35552_	Cluster Incl. AI041180:ov77e05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1643360 /clone_end=3 /gb=AI041180 at	PCYT1B	phosphate cytidylyltransferase 1, choline, Xp22.22

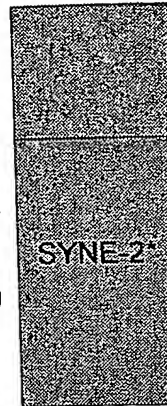
	/gi=3280374 /ug=Hs.132794 /len=810		beta isoform	
35766_	Cluster Incl. M26326:Human keratin 18 mRNA, complete cds /cds=(51,1343)	KRT18	keratin 18	12q13
at	/gb=M26326 /gi=186690 /ug=Hs.65114 /len=1412			
36021_	Cluster Incl. AL049409:Homo sapiens mRNA; cDNA DKFZp586H0919 (from clone DKFZp586H0919) /cds=UNKNOWN	LEF1	lymphoid enhancer-binding factor 1	4q23-q25
at	/gb=AL049409 /gi=4500194 /ug=Hs.44865 /len=1419			
36052_	Cluster Incl. U43959:Human beta 4 adducin mRNA, alternatively spliced partial cds /cds=(0,938) /gb=U43959 /gi=1172145	ADD2	adducin 2 (beta)	2p14-p13
at	/ug=Hs.4852 /len=1284			
36095_	Cluster Incl. N99340:IMAGE-20074 Homo sapiens cDNA /clone=IMAGE-20074	DKFZP586N1922	DKFZP586N1922 protein	19q13.1
at	/gb=N99340 /gi=1270755 /ug=Hs.7357 /len=1110			
36372_	Cluster Incl. U51333:Human hexokinase III (HK3) mRNA, complete cds /cds=(74,2845)	HK3	hexokinase 3 (white cell)	5q35.2
at	/gb=U51333 /gi=1255787 /ug=Hs.159237 /len=3049			
36464_	Cluster Incl. X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323	SGP28	specific granule protein (28 kDa)	6p12.3
at	/gi=1213612 /ug=Hs.54431 /len=2124			
36657_	Cluster Incl. AA883870:am26f01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1467961 /clone_end=3 /gb=AA883870	APOC2	apolipoprotein C-II	19q13.2
at	/gi=2993400 /ug=Hs.75615 /len=599			

36710_	Cluster Incl. Z38026:H.sapiens mRNA for FALL-39 peptide antibiotic /cds=(11,523) at /gb=Z38026 /gi=558378 /ug=Hs.51120 /len=615	CAMP	cathelicidin antimicrobial peptide	3p21.3
36780_	Cluster Incl. M25915:Human complement cytolysis inhibitor (CLI) mRNA, complete cds at /cds=(198,1544) /gb=M25915 /gi=180619 /ug=Hs.75106 /len=1651	CLU	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repressed prostate message 2, apolipoprotein J)	8p21-p12
38487_	Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) at /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777	FLJ12442	hypothetical protein FLJ12442	
38975_	Cluster Incl. AF062534:Homo sapiens genethonin 1 mRNA, complete cds at /cds=(127,1203) /gb=AF062534 /gi=3851521 /ug=Hs.109590 /len=2340	GENX-3414	genethonin 1	4q24-q25
39070_	Cluster Incl. U03057:Human actin bundling protein (HSN) mRNA, complete cds at /cds=(111,1592) /gb=U03057 /gi=458027 /ug=Hs.118400 /len=2767	SNL	singed (Drosophila)-like (sea urchin fascin homolog like)	7p22
39221_	Cluster Incl. AF004231:Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR cl-10) mRNA, complete cds	LILRB2	leukocyte immunoglobulin-like receptor,	19q13.4

	/cds=(208,2001) /gb=AF004231 /gi=2343110 /ug=Hs.22405 /len=2863		subfamily B (with TM and ITIM domains), member 2	
39307_ s_at	Cluster Incl. X81637:H.sapiens clathrin light chain b gene /cds=UNKNOWN /gb=X81637 /gi=963046 /ug=Hs.239782 /len=5938	CLTB	clathrin, light polypeptide	4q21-qter
39775_ at	Cluster Incl. X54486:Human gene for C1- inhibitor /cds=(60,1562) /gb=X54486 /gi=29534 /ug=Hs.151242 /len=1827	SERPINC1	complement component 1 inhibitor	11q12-q13.1
40282_ s_at	Cluster Incl. M84526:Human adipsin/complement factor D mRNA, complete cds /cds=(54,740) /gb=M84526 /gi=178625 /ug=Hs.155597 /len=1071	DF	D component of complement (adipsin)	19p13.3
40365_ at	Cluster Incl. M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891 /ug=Hs.73797 /len=2060	GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	19p13.3
40763_ at	Cluster Incl. U85707:Human leukemogenic homolog protein (MEIS1) mRNA, complete cds /cds=(65,1237) /gb=U85707 /gi=2058550 /ug=Hs.170177 /len=2511	MEIS1	Meis1 (mouse) homolog	2p14-p13
41045_ at	Cluster Incl. U77643:Homo sapiens K12 protein precursor mRNA, complete cds /cds=(118,864) /gb=U77643 /gi=2062390 /ug=Hs.95655 /len=2000	SECTM1	secreted and transmembrane 1	17q25
41448_ at	Cluster Incl. AC004080:Homo sapiens PAC clone DJ0170019 from 7p15-p21	HOXA10	homeo box A10	7p15-p14

at /cds=(0,1247) /gb=AC004080 /gi=2822164
/ug=Hs.110637 /len=1248

Cluster Incl. AL080133:Homo sapiens
mRNA; cDNA DKFZp434G173 (from clone
41815_ DKFZp434G173) /cds=(122,3400)
at /gb=AL080133 /gi=5262573 /ug=Hs.57749
/len=4307



synaptic nuclei

expressed

gene 2

14q23.2

Table 28a

classes	BM - t(8;21)	BM - t(15;17)	BM - inv(16)	BM - t(11q23)/ML L	BM - AML
accuracy	1.00	1.00	1.00	1.00	1.00
prediction strenght	0.88	0.91	0.99	0.89	0.89
Symbol	P(g,c) values	P(g,c) values	P(g,c) values	P(g,c) values	P(g,c) values
EPOR		7.36	7.36		2.74
unknown cDNA*		-6.46			
unknown cDNA*		-2.76			
LENG4*		-2.92			
CTSE		3.35		2.51	2.39
PGLYRP		7.39			
CSPG2		7.39			
H2AFN				-5.02	
IRH	-2.12				

IL18RAP				4.79	
CDKL2		-3.12			
PIG6		-2.92			
SSTR4		16.61			
LIG1					3.06
FCER2		4.72			
B3GAT3		-2.04			
LOC56928*				-8.39	-1.70
PCYT1B	3.56				
KRT18		-3.02			
LEF1				3.26	3.26
ADD2		5.63			
DKFZP586N192 2*			-8.84		
HK3		6.55			
SGP28*					3.04
APOC2		-5.33		-4.16	
CAMP		6.40			
CLU		-2.71			

FLJ12442*		-2.16			
GENX-3414*				1.97	
SNL		-3.64			
LILRB2		9.75			
CLTB				-4.38	
SERPING1		-2.48			
DF		-2.95			-1.73
GNA15		-2.69			
MEIS1				-4.22	
SECTM1		7.07			
HOXA10				-3.18	
SYNE-2*				3.36	

Table 28b: In total 269 cases with leukemia or normal bone marrow (BM) were analyzed. 248 of 269 (92.2%) cases were assigned to the correct leukemia type in all pairwise comparisons. The sensitivity indicated for each subgroup indicates the percentage of cases of the specific subgroup identified correctly in all pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

	ALL t(4;11)	ALL t(8;14)	ALL B not Ph	ALL Ph	T- ALL	AML +8	AML complex	AML normal	AML t(8;21)	AML t(15;17)	AML inv(16)	AML MLL	CLL	CML	normal BM	total	sensitivity %	specificity %
ALL t(4;11)	9															9	100.00	90.00
ALL t(8;14)		23						1								4	75.00	100.00
ALL B not Ph			8	1												9	88.89	80.00
ALL Ph			1	14												15	93.33	87.50
T-ALL					8			1								9	88.89	100.00
AML +8						6		4								10	0.60	100.00
AML complex	1						30	3							1	36	83.33	90.91
AML normal				1			1	58				2				62	93.55	85.29
AML t(8;21)									3							13	100.00	100.00
AML t(15;17)										20						20	100.00	100.00
AML inv(16)											12					12	100.00	100.00
AML												13				15	86.67	86.67
MLL													3			32	96.88	1.00
CLL														14		14	100.00	100.00
CML																9	100.00	90.00
normal BM																10		
total	10	3	10	16	8	6	33	68	13	20	12	15	31	14	10	269		

Table 28c: In total 3766 individual assignments of leukemia and normal bone marrow were analyzed. 3745 of 3766 assignments (99.4%) were correct. The sensitivity indicated for each subgroup indicates the percentage of correct assignments for cases of the specific subgroup in pairwise comparisons. The specificity indicates for each subgroup the percentage of correct assignments to this subgroup.

	ALL t(4;11)	ALL t(8;14)	ALL B not Ph	ALL B Ph	T- ALL	AML +8	AML complex	AML normal	AML t(8;21)	AML t(15;17)	AML inv(16)	AML MLL	CLL	CML	normal BM	total	sensitivity %	specificity %
ALL t(4;11)	126															126	100.00	99.21
ALL t(8;14)		56						1								56	98.21	100.00
ALL B not Ph			126	1												126	99.21	98.43
ALL B Ph				210												210	99.52	99.05
T-ALL					126			1								126	99.21	100.00
AML +8						136		4								140	97.14	100.00
AML complex	1			1			198	3							1	504	98.81	99.40
AML normal				1			1	868				2				868	99.54	98.86
AML t(8;21)									182							182	100.00	100.00
AML t(15;17)										280						280	100.00	100.00
AML inv(16)											168					168	100.00	100.00
AML MLL												210				210	99.05	99.05
CLL													447			448	99.78	100.00
CML														196		196	100.00	100.00
normal BM																126	100.00	99.21
total	127	55	127	211	125	136	501	874	182	280	168	210	447	196	127	3766		

Table 29

Analysis of the listed 14 leukemia subgroups and normal bone marrow (BM) according to the method as described by Golub et al. In pairwise comparison

	N
ALL t(4;11)	9
ALL t(8;14)	4
ALL B not Ph	9
ALL Ph	15
T-ALL	9
AML +8	10
AML complex	36
AML normal	62
AML t(8;21)	13
AML t(15;17)	20
AML inv(16)	12
AML MLL	15
CLL	32
CML	14
normal BM	9

ALL t(4;11) vs. all other		samples: 9 / 260		
accuracy	1			
confidence	0.983255511396901			
gene	signal-to-noise	p	decision limit	gene symbol
215925_s_at	2.15211119031413	0		
225592_at	2.10479676639873	0		NRM
205821_at	2.06781828794101	0		D12S2489E
209168_at	2.03682741085015	0		GPM6B
225563_at	2.0365845909197	0		
209170_s_at	1.99341681464758	0		GPM6B
219033_at	1.98127277039877	0*	3296.75	FLJ21308
227407_at	1.9806645400311	0*	2368.95	
226496_at	1.94883167321783	0		
219463_at	1.92861464656998	0		C20orf103
203796_s_at	1.90484126349741	0		BCL7A
210934_at	1.78273564893858	0		BLK
221969_at	1.72749112194125	0		PAX5
239393_at	1.72516948033426	0		
238750_at	1.71981673787555	0		
239214_at	1.67607810398359	0*	645.75	
218469_at	1.65073049955565	0		CKTSF1B1
226244_at	1.64755028976206	0		
218384_at	1.64357646019602	0		CRHSP-24
209815_at	1.64023870547228	0		PTCH

t(4;11) vs. t(15;17) samples: 9 / 20

accuracy 1

confidence 1

gene	signal-to-noise	p	decision limit	gene symbol
221969_at	5.83664657385464	0*	1301	PAX5
207697_x_at	5.35854600658567	0		LILRB2
203948_s_at	-5.11890143327711	0		MPO
224918_x_at	-4.9355306862525	0		MGST1
203949_at	-4.8364973202297	0		MPO
231736_x_at	-4.46563746824662	0		MGST1
235101_at	4.28876186377802	0		KIAA1014
202481_at	4.05195275593644	0		SDR1
219463_at	3.9253737114322	0		C20orf103
201540_at	3.81769665767171	0		FHL1
238583_at	-3.81099135622948	0		
205382_s_at	-3.80101585016411	0		DF
226878_at	3.74369099536436	0		
210934_at	3.72127171897839	0		BLK
226545_at	3.69021106148297	0		
38487_at	-3.54247992575908	0		FLJ12442
220798_x_at	-3.50808230625528	0		FLJ11535
232201_at	3.50091671488931	0		NKD2
204069_at	3.4252967216987	0		MEIS1
244261_at	3.40910490910101	0		

t(4;11) vs. inv(16)

samples: 9 / 12

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

225653_at

-6.57614058007186

0*

129.2

PAX5

221969_at

5.83664657385464

0

CCND2

231259_s_at

-5.68009935369819

0

MPO

203949_at

-4.47845706407372

0

CCND2

200951_s_at

-4.24994685464806

0

C20orf103

219463_at

3.9253737114322

0

MPO

203948_s_at

-3.82832616186979

0

CCND2

200953_s_at

-3.81507848947069

0

NET-6

217979_at

3.7506313191621

0

BLK

210934_at

3.72127171897839

0

RAB32

204214_s_at

-3.64249678228396

0

CEBPD

203973_s_at

-3.54203246324105

0

NKD2

232201_at

3.50091671488931

0

GDF11

216860_s_at

3.46199526723217

0

244261_at

3.40910490910101

0

CST3

201360_at

-3.40410310063102

0

226496_at

3.36372190983709

0

238824_at

3.31690199423555

0

217966_s_at

-3.29280071064851

0

C1orf24

38340_at

2.62428006100593

0

HIP12

ALL t(4;11) vs. AML MLL		samples: 9 / 15		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
221969_at	4.924403129677	0*	1534.5	PAX5
226795_at	4.12248256776444	0		
205821_at	4.05458217339808	0		D12S2489E
201360_at	-3.44934876199386	0		CST3
244261_at	3.40910490910101	0		
217979_at	3.33945130505483	0		NET-6
204215_at	3.27742574573237	0		MGC4175
211404_s_at	-3.1044343641572	0		APLP2
217223_s_at	3.09813118817326	0		
206255_at	3.06828641368978	0		BLK
214875_x_at	-2.95163557135368	0		APLP2
201828_x_at	-2.94392957130376	0		CXX1
208702_x_at	-2.9259192302265	0		APLP2
208456_s_at	2.83112443648876	0		RRAS2
219229_at	-2.78106365052986	0		SLC21A11
210487_at	2.65572482698711	0		DNTT
210192_at	2.63764031456982	0		ATP8A1
226496_at	2.63678458715383	0		
203796_s_at	2.63294411410401	0		BCL7A
212207_at	2.62364024475935	0		KIAA1025

ALL t(4;11) vs. CLL		samples: 9 / 32			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
210045_at	6.76734853184964	0*	142.15	IDH2	
204798_at	4.99101493214162	0		MYB	
225592_at	4.17686594916951	0		NRM	
202503_s_at	4.02396247600866	0		KIAA0101	
219463_at	3.9253737114322	0		C20orf103	
201540_at	3.7195174107357	0		FHL1	
226545_at	3.4985271993093	0			
223276_at	3.36058308258119	0		NID67	
209267_s_at	3.33868760455037	0		LOC64116	
201416_at	3.27673886279907	0		SOX4	
224710_at	3.27404618682988	0		RAB34	
218384_at	3.26299093107225	0		CRHSP-24	
209365_s_at	3.22987740485106	0		ECM1	
219869_s_at	3.18151227716348	0		LOC64116	
218942_at	-3.1335063798458	0		FLJ22055	
209825_s_at	3.12344649016037	0		UMPK	
201417_at	3.10175892236352	0			
238022_at	3.08645149251292	0			
212281_s_at	3.07915047956129	0		MAC30	
204069_at	3.04751039522855	0		MEIS1	

ALL t(4;11) vs. CML		samples: 9 / 14		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
221969_at	5.83664657385464	0*	1301	PAX5
207000_s_at	4.65703873448273	0		PPP3CC
212484_at	4.34689222808594	0		MTVR
201485_s_at	4.25216281704109	0		RCN2
204214_s_at	-4.24363288728321	0		RAB32
203796_s_at	4.18407933075926	0		BCL7A
218223_s_at	4.16804739438629	0		LOC51177
226795_at	4.12248256776444	0		
205821_at	4.05458217339808	0		D12S2489E
221755_at	3.99463418568195	0		
219463_at	3.9253737114322	0		C20orf103
202332_at	3.87997129184981	0		CSNK1E
210254_at	-3.85534735854191	0		
209619_at	3.77477243739775	0		CD74
226878_at	3.74369099536436	0		
205557_at	-3.71054014877636	0		BPI
225713_at	3.59398617666668	0		KIAA1898
206440_at	-3.54851691296324	0		VELI1
232201_at	3.50091671488931	0		NKD2
204215_at	3.43706276144109	0		MGC4175

ALL t(4;11) vs. normal BM

samples: 9 / 9

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

201828_x_at

-6.82241973614495

0*

285.3

CXX1

210045_at

6.76734853184964

0

IDH2

214950_at

6.24435639089538

0

237431_at

5.31661820706767

0

225792_at

-5.04037264761662

0

205624_at

-4.8793192574965

0

CPA3

201540_at

4.79436840204501

0

FHL1

204214_s_at

-4.53807365704691

0

RAB32

218916_at

4.52409549429394

0

FLJ23436

200832_s_at

-4.29237917192722

0

SCD

203796_s_at

4.18407933075926

0

BCL7A

205051_s_at

-4.13944949609416

0

KIT

202332_at

4.13816009401715

0

CSNK1E

228176_at

-4.13090953290361

0

226795_at

4.12248256776444

0

208754_s_at

4.00220842620578

0

NAP1L1

221755_at

3.99463418568195

0

228424_at

-3.92813180248343

0

NAALADASEL

219463_at

3.9253737114322

0

C20orf103

212967_x_at

3.92366867855542

0

NAP1L1

ALL t(4;11) vs. ALL t(8;14)		samples: 9 / 4			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
210045_at	6.76734853184964	0*	142.15	IDH2	
240106_at	6.10571301118426	0			
202853_s_at	-5.88804457870992	0		RYK	
242434_at	-5.60754470569171	0			
237431_at	5.31661820706767	0			
201540_at	4.94655082712075	0		FHL1	
215855_s_at	4.71299810202736	0			
212357_at	4.18767818184794	0		KIAA0280	
204798_at	4.12313508850913	0		MYB	
226795_at	4.12248256776444	0			
77508_r_at	4.0317985345148	0		FLJ23282	
46142_at	3.95748459279267	0		FLJ12681	
225277_at	3.7552029934786	0			
210934_at	3.72127171897839	0		BLK	
215537_x_at	3.53324247477066	0			
232201_at	3.50091671488931	0		NKD2	
214505_s_at	3.42260996379197	0		FHL1	
244261_at	3.40910490910101	0			
208614_s_at	3.34565043119022	0		FLNB	
210298_x_at	3.30171221592859	0.01		FHL1	

ALL t(4;11) vs. ALL B not Ph		samples: 9 / 9		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
237431_at	5.31661820706767	0*	49	
219033_at	3.19032095561144	0		FLJ21308
219463_at	2.69567768562793	0		C20orf103
204069_at	2.54127866831197	0		MEIS1
201105_at	2.30596776500018	0		LGALS1
200907_s_at	2.19034049161844	0		KIAA0992
242414_at	2.08870062415486	0		
222492_at	-2.04226084466602	0		FLJ21324
230441_at	-2.03717805375485	0		
235291_s_at	2.0210425168076	0		
225592_at	2.01329642963674	0		NRM
200906_s_at	1.9632986862999	0		
201153_s_at	1.93254941630797	0		MBNL
201152_s_at	1.93227192981893	0		MBNL
241985_at	-1.91875000661653	0		
213894_at	1.89533012552966	0		KIAA0960
243756_at	1.82938790694615	0		
225563_at	1.82046495626766	0		
232231_at	1.8138577510169	0		
240581_at	1.80942575017411	0		

ALL t(4;11) vs. ALL Ph

samples: 9 / 15

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

204069_at

3.31118886883646

0*

482.55

MEIS1

219033_at

3.24786485857293

0

FLJ21308

219463_at

2.78353259146178

0

C20orf103

221969_at

2.4416835946504

0

PAX5

201874_at

2.38057857279198

0

FLJ21047

209170_s_at

2.31526351178702

0

GPM6B

233500_x_at

2.23629715560156

0

LLT1

205899_at

2.23375311954146

0

CCNA1

242414_at

2.21567202901383

0

205821_at

2.10144186601662

0

D12S2489E

205055_at

2.04951650013049

0

ITGAE

209168_at

2.02899949049115

0

GPM6B

226939_at

1.99568402107224

0

209354_at

-1.9938191217443

0

TNFRSF14

200906_s_at

1.9632986862999

0

225563_at

1.88712595721941

0

237431_at

1.87880985981148

0

34210_at

-1.86187594200254

0

CDW52

202853_s_at

-1.84984316383277

0

RYK

209167_at

1.84829764568262

0

GPM6B

ALL t(4;11) vs. T-ALL

samples: 9 / 9

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

221969_at	5.83664657385464	0*	1301	PAX5
237431_at	5.31661820706767	0		
213772_s_at	4.80540935532116	0		GGA2
219463_at	3.9253737114322	0		C20orf103
210934_at	3.72127171897839	0		BLK
242292_at	-3.53231266693437	0		
226496_at	3.49024496949904	0		
244261_at	3.40910490910101	0		
205640_at	3.04306419050975	0		ALDH3B1
219033_at	3.03434195473282	0		FLJ21308
209168_at	3.02932118514235	0		GPM6B
205821_at	2.9956567374574	0		D12S2489E
235706_at	2.99518505957364	0		CPM
225592_at	2.98114633774562	0		NRM
225314_at	-2.87525509857994	0		
209170_s_at	2.832580891342	0		GPM6B
215925_s_at	2.79328349720245	0		
204069_at	2.67025815490556	0		MEIS1
210192_at	2.63764031456982	0		ATP8A1
217080_s_at	2.60699026264913	0		HOMER-2B

ALL t(4;11) vs. AML +8

samples: 9 / 10

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

201828_x_at

-4.66708459109445

0*

226.35

CXX1

221969_at

3.82090922998168

0

PAX5

244261_at

3.40910490910101

0

210024_s_at

-3.20983153576119

0

UBE2E3

219013_at

-3.19035252569463

0

FLJ21634

226496_at

3.13934828480165

0

205821_at

3.04595286153542

0

D12S2489E

219229_at

-3.04273361188054

0

SLC21A11

222422_s_at

-3.02123752629534

0

MGC10924

233138_at

2.95580347805273

0

206255_at

2.76163042569406

0

BLK

217979_at

2.7584725396168

0

NET-6

203796_s_at

2.72124988867035

0

BCL7A

214761_at

2.62282117562643

0

OAZ

227407_at

2.55763093921665

0

209365_s_at

2.53044674597142

0

ECM1

228379_at

2.52915026244479

0

204214_s_at

-2.51760565011465

0

RAB32

202626_s_at

-2.5141028457265

0

LYN

244876_at

2.46777854429452

0

ALL t(4;11) vs. AML complex		samples: 9 / 36			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
221969_at	4.27209531988207	0*	1815.1	PAX5	
210934_at	3.72127171897839	0		BLK	
244261_at	3.40910490910101	0			
219463_at	3.31691046444078	0		C20orf103	
206255_at	2.78386884086495	0		BLK	
226496_at	2.68550006340332	0			
209170_s_at	2.55250295984436	0		GPM6B	
209168_at	2.44311832949527	0		GPM6B	
215925_s_at	2.34663986373513	0			
226244_at	2.33002353009868	0			
219033_at	2.29968992798521	0		FLJ21308	
205821_at	2.2854186259635	0		D12S2489E	
232201_at	2.05970386931189	0		NKD2	
209167_at	2.05931372040727	0		GPM6B	
244876_at	2.04904743648645	0			
212658_at	-2.00156707557967	0		LHFPL2	
227407_at	1.9737052609863	0			
202853_s_at	-1.93859575890205	0		RYK	
203796_s_at	1.92961910857241	0		BCL7A	
214761_at	1.92608972571974	0		OAZ	

ALL t(4;11) vs. AML normal		samples: 9 / 62		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
221969_at	4.52880455396521	0*	1791.55	PAX5
210934_at	3.72127171897839	0		BLK
205821_at	2.95344549198955	0		D12S2489E
206255_at	2.91976312133621	0		BLK
226496_at	2.83306188482026	0		
215925_s_at	2.5921353451626	0		
244261_at	2.54559007441965	0		
244876_at	2.46777854429452	0		
203796_s_at	2.38175636157975	0		BCL7A
209815_at	2.31390268701643	0		PTCH
204215_at	2.24841200417248	0		MGC4175
227407_at	2.2323195471751	0		
214761_at	2.22867492056937	0		OAZ
226244_at	2.1571079710692	0		
225563_at	2.13989749649066	0		
225592_at	2.10215542418477	0		NRM
35974_at	2.05472986731736	0		LRMP
217979_at	2.03188116697557	0		NET-6
230292_at	2.02307533754428	0		
209168_at	2.01872981119451	0		GPM6B

ALL t(4;11)_vs. AML t(8;21)		samples: 9 / 13			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
212484_at	4.34689222808594	0*	121.4	MTVR	
221969_at	4.27496053785902	0		PAX5	
203796_s_at	4.18407933075926	0		BCL7A	
219463_at	3.9253737114322	0		C20orf103	
210934_at	3.72127171897839	0		BLK	
232201_at	3.50091671488931	0		NKD2	
244261_at	3.40910490910101	0			
204069_at	3.34624733362178	0		MEIS1	
204214_s_at	-3.30583121065186	0		RAB32	
225592_at	3.20386305207036	0		NRM	
206255_at	3.14140321370378	0		BLK	
212658_at	-3.07377549400227	0		LHFPL2	
226496_at	3.07152636043149	0			
233138_at	2.95580347805273	0			
227041_at	2.93637529041438	0			
212480_at	2.90213688157125	0		KIAA0376	
203795_s_at	2.86560617331268	0		BCL7A	
202853_s_at	-2.76308096012904	0		RYK	
203949_at	-2.76134156327152	0		MPO	
219033_at	2.72927502272681	0		FLJ21308	

AML t(15;17) vs. all other		samples: 20 / 249			
accuracy	1				
confidence	0.984095291727473				
gene	signal-to-noise	p	decision limit	gene symbol	
214450_at	2.5552572465358	0	5275.3	CTSW	
38487_at	2.48122703820417	0*		FLJ12442	
212953_x_at	2.383904085321	0		CALR	
224794_s_at	2.04094710734487	0		LOC51148	
221004_s_at	2.02822882303862	0	13772.15	ITM3	
204150_at	1.96620111034732	0		STAB1	
203948_s_at	1.77090499793556	0*		MPO	
219837_s_at	1.67874985207037	0		C17	
205382_s_at	1.63444144003612	0		DF	
241383_at	1.6305764545467	0			
216032_s_at	1.61454780261863	0		SDBCAG84	
200654_at	1.60202170245338	0		P4HB	
220798_x_at	1.58679638297009	0		FLJ11535	
208852_s_at	1.58602299942644	0		CANX	
203074_at	1.57040201174593	0		ANXA8	
200656_s_at	1.55688359776913	0		P4HB	
209344_at	1.55490125921714	0		TPM4	
205624_at	1.52362814764187	0		CPA3	
64942_at	1.52358978934783	0			
AFFX-					
HUMGAPDH/M33197_5_at	-				
HG-U133A	1.05449125226594	0		GAPD	

AML t(15;17) vs. AML inv(16)		samples: 20 / 12			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
204661_at	-3.70847055085953	0*	1899.15	CDW52	
209732_at	-3.23538966029247	0		CLECSF2	
241742_at	-3.11768531834572	0		PRAM-1	
38487_at	3.08138549900179	0		FLJ12442	
238022_at	3.0278549438122	0			
204563_at	-2.99471501611954	0		SELL	
34210_at	-2.99398735377828	0		CDW52	
203535_at	-2.97123029136408	0		S100A9	
217478_s_at	-2.93655072055469	0			
214450_at	2.92945546081029	0		CTSW	
211991_s_at	-2.91096104465505	0		HLA-DPA1	
208306_x_at	-2.87060964824031	0		HLA-DRB4	
213779_at	2.84856846381654	0			
211990_at	-2.76844422327205	0		HLA-DPA1	
221004_s_at	2.72545702224706	0		ITM3	
209312_x_at	-2.66880572066538	0		HLA-DRB1	
219789_at	-2.64334906817191	0		NPR3	
204425_at	-2.62831954360607	0		ARHGAP4	
205076_s_at	-2.59502309617401	0		CRA	
64942_at	2.28304127550384	0			

AML t(15;17) vs. AML MLL		samples: 20 / 15		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
205624_at	3.0741697102978	0*	2052.6	CPA3
38487_at	2.78111206643545	0		FLJ12442
203948_s_at	2.68497999695567	0		MPO
221004_s_at	2.64526084301972	0		ITM3
200951_s_at	2.52924582612911	0		CCND2
206761_at	2.52586949939666	0		TACTILE
203949_at	2.44678680592608	0		MPO
214651_s_at	-2.42192013365627	0		HOXA9
200952_s_at	2.39696270141848	0		CCND2
64942_at	2.28304127550384	0		
200953_s_at	2.24845652213108	0		CCND2
204150_at	2.2435902165197	0		STAB1
212953_x_at	2.22414089725316	0		CALR
233072_at	2.22380780245302	0		KIAA1857
214450_at	2.16984309325722	0		CTSW
224794_s_at	2.14479331910386	0		LOC51148
205349_at	2.12589700684588	0		GNA15
212509_s_at	2.11142192746438	0		
224839_s_at	2.07810412712239	0		GPT2
210788_s_at	2.07490438621852	0		LOC51635

AML t(15;17) vs. CLL		samples: 20 / 32			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
203949_at	6.8835946674069	0*	5834.85	MPO	
203948_s_at	5.89121269767824	0		MPO	
206871_at	4.93321162912793	0		ELA2	
226043_at	4.54092115946342	0		AGS3	
213854_at	4.34395164475566	0		SYNGR1	
224918_x_at	4.34201320024004	0		MGST1	
206111_at	4.19970662571818	0		RNASE2	
200654_at	4.03204616783544	0		P4HB	
231736_x_at	4.00585801175558	0		MGST1	
224838_at	-3.92476184954236	0			
211990_at	-3.92005265639026	0		HLA-DPA1	
238583_at	3.81099135622948	0			
221004_s_at	3.79791980511322	0		ITM3	
212400_at	-3.75779674692328	0			
211709_s_at	3.73806507086654	0		SCGF	
214575_s_at	3.66149641725929	0		AZU1	
205382_s_at	3.59180789007477	0		DF	
238022_at	3.5791572544895	0			
212953_x_at	3.54883221957949	0		CALR	
38487_at	3.51682772737691	0		FLJ12442	

AML t(15;17) vs. CML		samples: 20 / 14		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
201029_s_at	4.80190269912041	0*	4487.95	MIC2
212531_at	-4.73996757450677	0		LCN2
206676_at	-4.32531789709243	0		CEACAM8
216379_x_at	-4.27706524116979	0		
209771_x_at	-4.21950511119586	0		CD24
207269_at	-3.91601606801308	0		DEFA4
205557_at	-3.83288724786037	0		BPI
202018_s_at	-3.78757135021052	0		LTF
38487_at	3.67170603901023	0		FLJ12442
211657_at	-3.58933972989264	0		
205382_s_at	3.52725281328905	0		DF
220798_x_at	3.50808230625528	0		FLJ11535
209772_s_at	-3.45628903280328	0		CD24
221004_s_at	3.42707462770742	0		ITM3
203535_at	-3.38406746753723	0		S100A9
205863_at	-3.37594312179774	0		S100A12
204174_at	-3.3757799683273	0		ALOX5AP
203757_s_at	-3.33946937382462	0		CEACAM6
225386_s_at	-3.31814635286046	0		LOC92906
64942_at	2.28304127550384	0		

AML t(15;17) vs. normal BM		samples: 20 / 9			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
225792_at	-5.04037264761662	0*	76.45		
202018_s_at	-5.02314565371121	0		LTF	
223280_x_at	-4.43579892206636	0		MS4A6A	
212531_at	-4.09661809496392	0		LCN2	
203535_at	-3.97435355306196	0		S100A9	
205382_s_at	3.87917813251128	0		DF	
224356_x_at	-3.8624083855044	0		MS4A6A	
201029_s_at	3.64114093559717	0		MIC2	
219471_at	-3.59149059254273	0		FLJ21562	
223391_at	-3.55822107244772	0		LOC81537	
225897_at	-3.53074009879907	0			
209831_x_at	3.47754001947329	0		DNASE2	
230526_at	-3.32964763857134	0		FLJ20015	
221004_s_at	3.30073847019088	0		ITM3	
38487_at	3.26067308155523	0		FLJ12442	
207697_x_at	-3.24955398927113	0		LILRB2	
203645_s_at	-3.22408073656527	0		CD163	
201506_at	-3.1496662320639	0		TGFB1	
239278_at	-3.14559842984954	0			
201640_x_at	3.1436907617525	0		CLPTM1	

AML t(15;17) vs. ALL t(8;14)		samples: 20 / 4			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
212400_at	-6.34509116618667	0*	124.35	KIAA1842	
239835_at	-4.64446812677972	0		SYNGR1	
213854_at	4.34395164475566	0		ADAM19	
209765_at	-3.90392395971701	0		CALR	
212953_x_at	3.6338360358333	0		FLJ11535	
220798_x_at	3.50808230625528	0		FOXO1A	
202723_s_at	-3.43565959824609	0		DF	
205382_s_at	3.38600016039015	0		IDUA	
205059_s_at	3.37067676532123	0		FLJ12442	
38487_at	3.30566285802216	0			
235823_at	-3.22388670008998	0		CTSW	
214450_at	3.19435746487831	0		CLPTM1	
201640_x_at	3.1436907617525	0		SYNE-2	
242774_at	-3.10884740483827	0		CPA3	
205624_at	3.08135190030361	0		ITM3	
221004_s_at	3.04980072799641	0		DDAH2	
202262_x_at	3.00631284337625	0		LOC113263	
227525_at	-2.99175282480629	0		BACH2	
227173_s_at	-2.97620214103741	0		FLJ12681	
46142_at	2.45069282884032	0			

AML t(15;17) vs. ALL B not Ph samples: 20 / 9

accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
205382_s_at	3.94103663553541	0*	3034.4	DF
214450_at	3.7272017152315	0		CTSW
220798_x_at	3.50808230625528	0		FLJ11535
209831_x_at	3.47754001947329	0		DNASE2
212953_x_at	3.01141919123014	0		CALR
231736_x_at	2.98271279100376	0		MGST1
211990_at	-2.92818453065756	0		HLA-DPA1
241383_at	2.90001109867359	0		
224918_x_at	2.89999004151056	0		MGST1
205624_at	2.84403833450845	0		CPA3
38487_at	2.72794873611638	0		FLJ12442
200654_at	2.71316195189784	0		P4HB
221004_s_at	2.68426024071363	0		ITM3
208689_s_at	2.62363368134519	0		RPN2
221739_at	2.61870113363546	0		IL27
203679_at	2.54794444503946	0		IL1RL1LG
217716_s_at	2.27011720191064	0		SEC61A1
208852_s_at	2.24073987327423	0		CANX
220744_s_at	2.21509524546031	0		WDR10
55093_at	1.63667373135171	0		KIAA1402

AML t(15;17) vs. ALL Ph		samples: 20 / 15			
accuracy		1			
confidence		1			
gene	signal-to-noise	p	decision limit	gene symbol	
211990_at	-3.8327925790289	0	41	HLA-DPA1	
220798_x_at	3.50808230625528	0*		FLJ11535	
224918_x_at	3.50754573671859	0		MGST1	
214450_at	3.50155234311803	0		CTSW	
231736_x_at	3.3802502122888	0		MGST1	
205624_at	3.21024990481945	0		CPA3	
203373_at	-3.1946557461653	0		STAT2	
205382_s_at	3.14485336319038	0		DF	
212953_x_at	2.86696122083705	0		CALR	
203948_s_at	2.80859584810434	0		MPO	
238583_at	2.78542343697266	0			
209732_at	-2.73475243434259	0		CLECSF2	
233072_at	2.63743334734262	0		KIAA1857	
209619_at	-2.55642326842901	0		CD74	
226545_at	-2.50061887472005	0			
238022_at	2.48587783472615	0			
210487_at	-2.48460923232205	0		DNTT	
200654_at	2.41521499865532	0		P4HB	
209831_x_at	2.34522293184427	0		DNASE2	
225790_at	2.31674527318944	0			

AML t(15;17) vs. T-ALL

samples: 20 / 9

accuracy

1

confidence

1

gene	signal-to-noise	p	decision limit	gene symbol
203949_at	5.76493681986315	0*	6205	MPO
203948_s_at	5.52731611865475	0		MPO
224918_x_at	5.05683576581082	0		MGST1
231736_x_at	4.44324813542895	0		MGST1
213854_at	4.34395164475566	0		SYNGR1
205382_s_at	4.13724322163424	0		DF
206871_at	4.09729897232645	0		ELA2
206111_at	3.61313451786675	0		RNASE2
242292_at	-3.53231266693437	0		
214575_s_at	3.51522052980985	0		AZU1
220798_x_at	3.50808230625528	0		FLJ11535
38487_at	3.40780715783254	0		FLJ12442
200654_at	3.36034425167829	0		P4HB
235101_at	-3.27592263847035	0		KIAA1014
208689_s_at	3.18547214467073	0		RPN2
212953_x_at	3.18316032369792	0		CALR
204348_s_at	3.06277487805438	0		AK3
201537_s_at	2.82382291089523	0		DUSP3
214450_at	2.81907045269144	0		CTSW
204150_at	2.73329912927614	0		STAB1

AML t(15;17) vs. AML +8		samples: 20 / 10			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
214450_at	3.0865086945171	0*	1926.7	CTSW	
212953_x_at	2.71319553382926	0		CALR	
236787_at	2.4273500798775	0			
200952_s_at	2.39696270141848	0		CCND2	
205624_at	2.38480346275743	0		CPA3	
38487_at	2.38251622694176	0		FLJ12442	
205614_x_at	2.24846130719191	0		MST1	
206761_at	2.20501899975366	0		TACTILE	
216320_x_at	2.16690689445934	0			
224794_s_at	2.14479331910386	0		LOC51148	
233072_at	2.07721746169547	0		KIAA1857	
221004_s_at	2.05892662897696	0		ITM3	
227326_at	2.04924504239987	0			
221980_at	2.01752809990056	0			
225547_at	-1.98126007880124	0			
210145_at	-1.95455412087558	0		PLA2G4A	
212509_s_at	1.92046303571342	0			
209344_at	1.90906303754685	0		TPM4	
201029_s_at	1.87538506046111	0		MIC2	
204150_at	1.87343002266891	0		STAB1	

AML t(15;17) vs. AML

complex samples: 20 / 36

accuracy 1

confidence 1

gene	signal-to-noise	p	decision limit	gene symbol
205382_s_at	2.47024872277389	0		DF
212953_x_at	2.44599456599903	0*	4652.35	CALR
64942_at	2.28304127550384	0		
214450_at	2.2627370518124	0		CTSW
38487_at	2.15395063071356	0		FLJ12442
224794_s_at	2.14479331910386	0		LOC51148
220798_x_at	2.06303065394458	0		FLJ11535
216032_s_at	2.05259440043708	0		SDBCAG84
203948_s_at	2.04245448483567	0		MPO
209732_at	-1.90630142681759	0		CLECSF2
230526_at	-1.90204644112897	0		FLJ20015
238022_at	1.89121106100583	0		
200654_at	1.73209407132843	0		P4HB
204150_at	1.72000809746397	0		STAB1
213447_at	-1.71480861978241	0		IPW
206847_s_at	-1.68023930751716	0		HOXA7
203074_at	1.65576107663154	0		ANXA8
219837_s_at	1.65191807395586	0		C17
200931_s_at	-1.6356222023809	0		VCL
AFFX-				
HUMGAPDH/M33197_5_at	-			
HG-U133A	1.15678566237816	0		GAPD

AML t(15;17) vs. AML normal samples: 20 / 62

accuracy 1

confidence 1

gene	signal-to-noise	p	decision limit	gene symbol
212953_x_at	2.64618373092816	0*	4541.1	CALR
214450_at	2.28653040002124	0		CTSW
203948_s_at	2.28093863578688	0		MPO
38487_at	2.27897339525457	0		FLJ12442
224794_s_at	2.14479331910386	0		LOC51148
233072_at	2.02319157581908	0		KIAA1857
221004_s_at	2.01169552990941	0		ITM3
236787_at	1.97410536661333	0		
209732_at	-1.93278822451406	0		CLECSF2
214651_s_at	-1.88045707977072	0		HOXA9
216032_s_at	1.84310066944834	0		SDBCAG84
227326_at	1.83154138034996	0		
200952_s_at	1.79422847402715	0		CCND2
208852_s_at	1.77896258332914	0		CANX
200654_at	1.77731955574697	0		P4HB
204150_at	1.77067560905128	0		STAB1
64942_at	1.71976456537364	0		
203949_at	1.69386661503752	0		MPO
235753_at	-1.67072227461966	0		
209344_at	1.65496211687573	0		TPM4

AML t(15;17) vs. AML t(8;21)		samples: 20 / 13			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
214450_at	3.53862069365814	0*	1809.95	CTSW	
38487_at	3.30334484935728	0		FLJ12442	
209732_at	-3.18277220746091	0		CLECSF2	
204150_at	2.73329912927614	0		STAB1	
201596_x_at	2.73162867034962	0		KRT18	
213944_x_at	2.5862372690463	0			
230526_at	-2.42276930706474	0		FLJ20015	
212509_s_at	2.33481477262277	0			
211990_at	-2.3270695509372	0		HLA-DPA1	
204319_s_at	-2.25060861801642	0		RGS10	
205614_x_at	2.24846130719191	0		MST1	
216320_x_at	2.16690689445934	0			
224794_s_at	2.14479331910386	0		LOC51148	
224839_s_at	2.07810412712239	0		GPT2	
227326_at	2.04924504239987	0			
238365_s_at	2.03674279873081	0			
228827_at	-2.03460798747208	0			
228570_at	2.03169244854036	0			
205349_at	2.02142471684528	0		GNA15	
200986_at	2.01484061650733	0		SERPING1	

AML inv(16) vs. all other		samples: 12 / 257			
accuracy	1				
confidence	0.786321619312236				
gene	signal-to-noise	p	decision limit	gene symbol	
201497_x_at	1.74852845185764	0		MYH11	
231310_at	1.47164364462932	0			
241525_at	1.40464277333052	0			
233555_s_at	1.36141951191384	0*	462.05		
224724_at	1.35707926936144	0		KIAA1247	
200665_s_at	1.34209700274375	0		SPARC	
202370_s_at	-1.29245470192814	0		CBFB	
222862_s_at	1.26048366428059	0		AK5	
200675_at	-1.23914248971997	0		CD81	
205076_s_at	1.22017942852008	0		CRA	
201496_x_at	1.21510481759962	0		MYH11	
223385_at	1.2113380867898	0		CYP2S1	
221486_at	-1.19152063013451	0			
223471_at	-1.18312106893472	0			
206135_at	1.18181935093584	0		KIAA0535	
206956_at	1.17922310970084	0		BGLAP	
235359_at	1.16409001423194	0			
202016_at	1.15872909212242	0*	1	MEST	
201324_at	1.15017496156271	0		EMP1	
AFFX-HUMRGE/M10098_5_at					
- HG-U133B	0.737113176900438	0			

AML inv(16) vs. AML MLL		samples: 12 / 15			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
200951_s_at	4.24994685464806	0*	75.6	CCND2	
228058_at	3.25212044058077	0			
219271_at	2.57049778814556	0		FLJ12691	
231259_s_at	2.43255056573718	0		CCND2	
214651_s_at	-2.30388406553935	0		HOXA9	
202551_s_at	2.25890379783091	0		CRIM1	
205453_at	2.23059959679219	0		HOXB2	
200953_s_at	2.19700687874039	0		CCND2	
213737_x_at	-2.16186095833837	0			
235818_at	2.13054793207832	0			
225653_at	2.10834669134201	0			
232636_at	-2.07022186491858	0			
202746_at	2.06211630393441	0			
200665_s_at	2.03751489015447	0		SPARC	
203949_at	2.01364277991339	0		MPO	
202552_s_at	1.96670486082105	0		CRIM1	
223471_at	-1.96529988161274	0			
201828_x_at	-1.9593150488894	0		CXX1	
235359_at	1.95403665761428	0			
202747_s_at	1.9384101680124	0		ITM2A	

AML inv(16) vs. CLL

samples: 12 / 32

accuracy

1

confidence

1

gene	signal-to-noise	p	decision limit	gene symbol
203949_at	6.95021247410033	0*	3746.5	MPO
211709_s_at	5.18681505358433	0		SCGF
203948_s_at	4.72760268663435	0		MPO
231310_at	4.35158499850242	0		
226043_at	4.31805631251135	0		AGS3
201417_at	3.83165504179581	0		
209365_s_at	3.8293529362527	0		ECM1
224838_at	-3.72164043642693	0		
243000_at	3.63182045730937	0		
223382_s_at	3.56679694464951	0		NIN283
201163_s_at	3.21223463217947	0		IGFBP7
202862_at	3.20454480816595	0		FAH
231982_at	3.1934694742924	0		
201162_at	3.15702502490111	0		IGFBP7
218942_at	-3.1335063798458	0		FLJ22055
212827_at	-3.11017349120191	0		IGHM
224710_at	3.04332806808412	0		RAB34
208864_s_at	3.01671716600197	0		TXN
211787_s_at	2.90916234544607	0		EIF4A1
205382_s_at	2.90564641349051	0		DF

AML inv(16).vs. CML		samples: 12 / 14		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
201029_s_at	4.31890554977499	0*	4017	MIC2
209365_s_at	3.8293529362527	0		ECM1
226844_at	3.75460881300519	0		
209771_x_at	-3.55889840129944	0		CD24
206440_at	-3.54851691296324	0		VELL1
233138_at	3.4735123827114	0		
216379_x_at	-3.43948341863688	0		
227749_at	3.41648620394084	0		
209772_s_at	-3.3477199485593	0		CD24
210982_s_at	3.24778523856649	0		HLA-DRA
218942_at	-3.24708603988632	0		FLJ22055
206676_at	-3.24497920147189	0		CEACAM8
204661_at	3.10482803895821	0		CDW52
212531_at	-3.09841450182506	0		LCN2
208306_x_at	3.05465357697194	0		HLA-DRB4
208890_s_at	2.99789197915585	0		PLXNB2
216015_s_at	2.9548034027314	0		
223839_s_at	-2.95162251991881	0		
207802_at	-2.93213346323135	0		SGP28
34210_at	2.86220111493221	0		CDW52

AML inv(16) vs. normal BM		samples: 12 / 9		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
225792_at	-5.04037264761662	0*	76.45	
224975_at	-5.01918026903577	0		NFIA
224976_at	-4.534006778733	0		NFIA
238652_at	4.21116590562832	0		
209365_s_at	3.8293529362527	0		ECM1
223044_at	-3.73370982362517	0		SLC11A3
226326_at	-3.6960030140107	0		
200832_s_at	-3.67575949264708	0		SCD.
213288_at	-3.55635098156803	0		
230988_at	-3.46948918999612	0		
205382_s_at	3.29073930292859	0		DF
201417_at	3.27682718704937	0		
225897_at	-3.21286424500781	0		
226299_at	3.21097313269574	0		pknbeta
210933_s_at	3.17596755096177	0		MGC4655
218094_s_at	3.1307319856851	0		C20orf35
201029_s_at	3.10235325372561	0		MIC2
210036_s_at	-3.09612221936927	0		KCNH2
212667_at	3.07883651171274	0		SPARC
40189_at	2.32056421839438	0		SET

AML inv(16) vs. ALL t(8;14)		samples: 12 / 4			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
214558_at	5.11198812058407	0*	75.15	GPR12	
227525_at	-4.9287188464128	0		LOC113263	
211852_s_at	4.75980688856888	0		ATRN	
238652_at	4.21116590562832	0			
206090_s_at	4.11779253006199	0		DISC1	
237864_at	3.94349147195948	0			
225051_at	-3.89930170229982	0			
209365_s_at	3.8293529362527	0		ECM1	
223382_s_at	3.56679694464951	0		NIN283	
201278_at	3.38592358815787	0		DAB2	
219654_at	3.25519407914616	0		PTPLA	
202074_s_at	-3.24311911278957	0		OPTN	
231982_at	3.1934694742924	0			
231310_at	3.18344789439715	0			
210933_s_at	3.17596755096177	0		MGC4655	
222062_at	3.12204176758762	0		WSX1	
242774_at	-3.10884740483827	0		SYNE-2	
244257_at	3.09069018899455	0			
212667_at	3.07883651171274	0		SPARC	
225305_at	2.99842864962803	0			

AML inv(16) vs. ALL B not Ph samples: 12 / 9

accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
205382_s_at	3.44559828536398	0*	2092.2	DF
206772_at	3.36924689882826	0		PTHR2
228058_at	3.25212044058077	0		
218094_s_at	3.1307319856851	0		C20orf35
223385_at	3.07706676910952	0		CYP2S1
204858_s_at	2.96720397750981	0		ECGF1
227556_at	2.66258700650327	0		ATP1B1
212463_at	-2.65372355495687	0		
201360_at	2.63414688358486	0		CST3
205997_at	2.6308573171159	0		ADAM28
231310_at	2.60181313279404	0		
203973_s_at	2.4714469340582	0		CEBPD
200872_at	2.42523459110761	0		S100A10
200661_at	2.42407433324859	0		PPGB
227415_at	-2.35663515228965	0		
219358_s_at	2.31004642323513	0		CENTA2
202016_at	2.30727907426241	0		MEST
208248_x_at	2.27797183411701	0		APLP2
212188_at	2.26974263089413	0		LOC115207
205076_s_at	2.257959447417	0		CRA

AML inv(16) vs. ALL Ph

samples: 12 / 15

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

231310_at

3.26954611223081

0*

119.2

STAT12

203373_at

-3.07194642697668

0

DNTT

210487_at

-2.57922739606335

0

ABCG2

209735_at

-2.57442202182339

0

MGC11352

223314_at

-2.46037319479876

0

TEM7R

227276_at

2.31171718422321

0

DF

205382_s_at

2.30057319708762

0

S100A10

200872_at

2.27656979916265

0

CD59

200985_s_at

-2.25258857041194

0

SIGLEC7

207224_s_at

2.24976284058658

0

APLP2

208702_x_at

2.21820176325777

0

CYP2E

209975_at

2.21237181448127

0

LOC64174

219452_at

2.18614057488219

0

MGST1

224918_x_at

2.18042008960618

0

PPGB

200661_at

2.15820911658542

0

CRA

205076_s_at

2.1576215121228

0

TIMM44

203092_at

-2.1346943506478

0

NET-6

217979_at

-2.13131555913964

0

PIG3

228058_at

2.11586185512013

0

210609_s_at

2.1104858897821

0

AML inv(16) vs. T-ALL

samples: 12 / 9

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

203949_at

5.55902965521097

0*

4116.65

MPO

205640_at

4.30508511818292

0

ALDH3B1

203948_s_at

4.299250186967

0

MPO

204484_at

-3.92079658637056

0

PIK3C2B

223482_at

3.8867405806948

0

TMPIT

205382_s_at

3.78294993092265

0

DF

242292_at

-3.53231266693437

0

224918_x_at

3.39770561886615

0

MGST1

228058_at

3.25212044058077

0

210314_x_at

3.15624540914219

0

TNFSF13

216015_s_at

2.9548034027314

0

206380_s_at

2.92913137540268

0

PFC

202944_at

2.90807873450708

0

NAGA

231736_x_at

2.90529949191742

0

MGST1

209500_x_at

2.88541455460133

0

TNFSF13

205312_at

2.86437379660673

0

SPI1

211495_x_at

2.85808523976773

0

TNFSF13

211101_x_at

2.82479786118477

0

LILRA2

219763_at

2.71839322196283

0

KIAA1608

225510_at

2.68685955542078

0

CHN1

AML inv(16) vs. AML +8		samples: 12 / 10		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
233138_at	3.4735123827114	0*	54.25	
209365_s_at	3.00986865470169	0		ECM1
202283_at	2.6160707896185	0		SERPINF1
218942_at	-2.45751904192227	0		FLJ22055
201828_x_at	-2.21365274281998	0		CXX1
200951_s_at	2.02357943949022	0		CCND2
226120_at	-2.01082485261142	0		LOC123016
203188_at	-1.9379696222037	0		B3GNT6
202085_at	-1.9147903697218	0		TJP2
206135_at	1.90877055638373	0		KIAA0535
210024_s_at	-1.90335978018863	0		UBE2E3
204661_at	1.83776082826379	0		CDW52
241525_at	1.83006374766269	0		
208710_s_at	-1.80896001968559	0		AP3D1
34210_at	1.75572696362264	0		CDW52
201497_x_at	1.74852845185764	0		MYH11
212236_x_at	1.74679406476776	0		
213810_s_at	1.69077455623534	0		FLJ10342
212250_at	-1.62885302351785	0		
AFFX-r2-Hs18SrRNA-5_at	-			
HG-U133A	1.32018767826727	0		

AML inv(16) vs. AML complex samples: 12 / 36

accuracy	1			
confidence	0.957308305034528			
gene	signal-to-noise	p	decision limit	gene symbol
203092_at	-1.77664454556306	0		TIMM44
209190_s_at	1.75723541848141	0*	1593.8	DIAPH1
201497_x_at	1.74852845185764	0*	134.75	MYH11
205076_s_at	1.73951655525411	0		CRA
241525_at	1.71682483225979	0		
213779_at	-1.71354352282537	0		
210982_s_at	1.70318998731519	0		HLA-DRA
200985_s_at	-1.64643993864436	0		CD59
212463_at	-1.6457941052799	0		
200675_at	-1.61546783522649	0*	707.85	CD81
218942_at	-1.59347299102441	0		FLJ22055
200984_s_at	-1.56833724351535	0		CD59
208894_at	1.54975491884609	0		HLA-DRA
202265_at	-1.53139324627965	0		BMI1
224724_at	1.5143785002027	0		KIAA1247
210715_s_at	-1.49004107536748	0		SPINT2
213452_at	-1.48522101377482	0		ZNF184
205382_s_at	1.45942422076027	0		DF
201360_at	1.45905524413008	0		CST3
206135_at	1.45729112913321	0		KIAA0535

AML inv(16) vs. AML normal		samples: 12 / 62			
accuracy	1				
confidence	0.952958978230212				
gene	signal-to-noise	p	decision limit	gene symbol	
200951_s_at	1.82916486676122	0		CCND2	
209365_s_at	1.79092214915991	0*	390.9	ECM1	
214651_s_at	-1.77796050968374	0*	187.6	HOXA9	
201497_x_at	1.74852845185764	0		MYH11	
231310_at	1.62450567760929	0*	167.8		
223385_at	1.57142154491015	0		CYP2S1	
206135_at	1.54931600211688	0		KIAA0535	
235753_at	-1.54691446076282	0			
231259_s_at	1.52681305174601	0		CCND2	
204661_at	1.46205490369508	0		CDW52	
202370_s_at	-1.45859936190513	0		CBFB	
213353_at	-1.44758735114725	0		ABCA5	
209905_at	-1.42239381454703	0		HOXA9	
200675_at	-1.38662888859944	0		CD81	
207194_s_at	1.38591797740996	0		ICAM4	
201324_at	1.36182933080382	0		EMP1	
235818_at	1.35992709972839	0			
225510_at	1.35514122232308	0		CHN1	
228834_at	1.35066870620531	0		TOB1	
34210_at	1.33546826742244	0		CDW52	

AML inv(16) vs. AML t(8;21)		samples: 12 / 13			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
233138_at	3.4735123827114	0*	54.25		
202283_at	2.6160707896185	0		SERPINF1	
201596_x_at	2.55517188589615	0		KRT18	
233555_s_at	2.48943541958708	0			
226818_at	2.3621676751726	0			
212828_at	2.33130605042964	0		SYNJ2	
227276_at	2.31171718422321	0		TEM7R	
224724_at	2.30850265580909	0		KIAA1247	
224764_at	2.25934489179779	0		ARHGAP10	
224049_at	2.25244855640038	0		KCNK17	
205453_at	2.23059959679219	0		HOXB2	
226841_at	2.21329419316194	0			
209975_at	2.21237181448127	0		CYP2E	
205076_s_at	2.21083117233863	0		CRA	
202340_x_at	2.18671963481275	0		NR4A1	
210314_x_at	2.17138407196792	0		TNFSF13	
34689_at	2.16463995293403	0		TREX1	
235359_at	2.12423469465025	0			
212188_at	2.11590883979512	0		LOC115207	
205718_at	2.10547132123535	0		ITGB7	

AML MLL vs. all other

samples: 15 / 254

accuracy

0.977695167286245

confidence.

0.736329320600874

failed:

3,6,7,11,155,212

gene	signal-to-noise	p	decision limit	gene symbol
228083_at	1.21941234348391	0		
201105_at	1.20839678060713	0*	8795.05	LGALS1
205849_s_at	1.03753805567643	0		UQCRB
205472_s_at	1.03076838857205	0		DACH
208702_x_at	1.01256627546813	0		APLP2
225700_at	-1.01092153300039	0		
222982_x_at	-1.00741126543277	0*	1101	SLC38A2
238856_s_at	-0.990415633837559	0*	1	
214875_x_at	0.989164186017564	0		APLP2
209616_s_at	0.966839890517189	0		CES1
205471_s_at	0.957394713027089	0		DACH
211404_s_at	0.942572231076861	0		APLP2
213857_s_at	-0.933745825960995	0		CD47
204951_at	-0.925961455918277	0		ARHH
203544_s_at	-0.922231323262765	0		STAM
204082_at	0.910815804799754	0		PBX3
219360_s_at	0.902459945140701	0		TRPM4
235604_x_at	-0.895150647295372	0		
200742_s_at	0.89214325035062	0		CLN2
217520_x_at	0.891291087387708	0		

AML MLL vs. CLL		samples: 15 / 32		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
224838_at	-3.80748815117863	0*	1810.6	
212400_at	-2.86025920523167	0		
212827_at	-2.83572202473321	0		IGHM
223514_at	-2.79698500849851	0		CARD11
207168_s_at	2.78000663400662	0		H2AFY
208456_s_at	-2.77288752188536	0		RRAS2
206111_at	2.74648404080317	0		RNASE2
204951_at	-2.73367910105826	0		ARHH
204215_at	-2.70725768797715	0		MGC4175
41220_at	-2.64744893915855	0		MSF
227173_s_at	-2.60156567650878	0		BACH2
211404_s_at	2.58701495228114	0		APLP2
201163_s_at	2.58627447208644	0		IGFBP7
227829_at	-2.5720529437702	0		
202880_s_at	-2.55714780536776	0		PSCD1
224837_at	-2.52465899436623	0		FOXP1
209374_s_at	-2.50451803785685	0		IGHM
243780_at	-2.49073709912546	0		
212590_at	-2.45765382458849	0		
AFFX-				
HUMGAPDH/M33197_3_at	-			
HG-U133B	2.15372303795555	0		GAPD

AML MLL vs. CML

samples: 15 / 14

accuracy

1

confidence

1

gene	signal-to-noise	p	decision limit	gene symbol
209771_x_at	-4.47855739740896	0*	4909	CD24
216379_x_at	-4.47782401977517	0		
212531_at	-4.20914790815671	0		LCN2
206676_at	-4.08016979869995	0		CEACAM8
205557_at	-3.89666780981116	0		BPI
209772_s_at	-3.7540800038095	0		CD24
211657_at	-3.35563391812807	0		
203757_s_at	-3.27728001846237	0		CEACAM6
202018_s_at	-3.2413562747036	0		LTF
205513_at	-3.11724133997788	0		TCN1
207269_at	-3.04676950166614	0		DEFA4
207802_at	-2.84753376114576	0		SGP28
236908_at	-2.83593202717857	0		
266_s_at	-2.75915771343774	0		CD24
201105_at	2.73676787442809	0		LGALS1
208890_s_at	2.63909820141829	0		PLXNB2
210244_at	-2.58291056673136	0		CAMP
214875_x_at	2.54486223713713	0		APLP2
236979_at	-2.51234802423843	0		
49306_at	1.35686961755716	0		AD037

AML MLL vs. normal BM		samples: 15 / 9			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
225792_at	-5.04037264761662	0*	76.45		
227812_at	-4.50172833847856	0			
236908_at	-4.3851399912751	0			
225700_at	-4.20778530270981	0			
202018_s_at	-4.1218976881036	0		LTF	
225804_at	3.78433665952281	0			
212531_at	-3.62189836886899	0		LCN2	
208651_x_at	-3.08131561292721	0		CD24	
209771_x_at	-2.80531442593767	0		CD24	
216379_x_at	-2.74718662648409	0			
210244_at	-2.74600903663689	0		CAMP	
226301_at	-2.70321745971481	0		dJ55C23.6	
227151_at	2.68181697471281	0			
209160_at	-2.64474285212333	0		AKR1C3	
225285_at	-2.56569832423798	0			
235818_at	-2.5546546541523	0			
226726_at	-2.52741579223109	0		LOC129642	
207269_at	-2.43598973973471	0		DEFA4	
226751_at	-2.41273912703748	0		DKFZP566K1924	
58780_s_at	1.24593648437062	0		FLJ10357	

AML MLL vs. ALL t(8;14)		samples: 15 / 4		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
227173_s_at	-2.97620214103741	0*	93.35	BACH2
225700_at	-2.97113581211542	0		
212400_at	-2.91449782508721	0		
227151_at	2.68181697471281	0		
205690_s_at	-2.63484847538673	0		G10
231552_at	2.60340424456959	0		
239647_at	2.56381751217569	0		
239835_at	-2.49692099181388	0		KIAA1842
226435_at	2.38716130768923	0		
226301_at	-2.38404537685874	0		dJ55C23.6
226607_at	2.34518225140996	0		L3MBTL
215785_s_at	-2.31901965008779	0		CYFIP2
225085_at	2.24977026547419	0		
214651_s_at	2.24855870756181	0		HOXA9
209765_at	-2.20363939375933	0		ADAM19
236606_at	-2.19711183569464	0		
218319_at	-2.1925818315627	0		PELI1
227525_at	-2.16383106825606	0		LOC113263
212538_at	-2.11358391570231	0		KIAA1058
228083_at	2.10218682980016	0		

AML MLL vs. ALL B not Ph		samples: 15 / 9		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
201482_at	2.87636338319455	0*	363.95	QSCN6
201105_at	2.64910601922115	0		LGALS1
239647_at	2.56381751217569	0		
211404_s_at	2.31189269578112	0		APLP2
201360_at	2.27456235196276	0		CST3
214875_x_at	2.20140608739693	0		APLP2
266_s_at	-2.19196810995278	0		CD24
208702_x_at	2.17966631844281	0		APLP2
223469_at	2.13015217253256	0		MGC10812
209771_x_at	-2.12750959401045	0		CD24
208248_x_at	2.10716186347527	0		APLP2
230441_at	-2.03717805375485	0		
200742_s_at	2.01183913393136	0		CLN2
216379_x_at	-1.97574478072792	0		
204215_at	-1.96532146024999	0		MGC4175
208650_s_at	-1.93906624919753	0		CD24
214651_s_at	1.92853927147488	0		HOXA9
233813_at	-1.8799760260639	0		
208703_s_at	1.86864966354898	0		APLP2
58780_s_at	1.40471564488899	0		FLJ10357

AML MLL vs. ALL Ph		samples: 15 / 15			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
210487_at	-2.66400596339357	0		DNTT	
211404_s_at	2.5799328562955	0		APLP2	
214875_x_at	2.53091704146699	0		APLP2	
208702_x_at	2.442063176235	0		APLP2	
214651_s_at	2.38931027314895	0		HOXA9	
234107_s_at	2.17019003130007	0*	321.6	LGALS1	
201105_at	2.08770407459668	0			
239647_at	2.02467198705529	0		NET-6	
217979_at	-1.99927745769533	0		HOXA10	
213150_at	1.98436589229381	0		D2S448	
212012_at	-1.96026252932157	0		KIAA0582	
207971_s_at	-1.95442302553682	0		CLN2	
200742_s_at	1.93172870108821	0			
236606_at	-1.90758120714248	0			
235753_at	1.89768662161529	0		H4FH	
232035_at	-1.87493486925109	0		MSF	
41220_at	-1.84432301556426	0		CD24	
209771_x_at	-1.83370834497243	0		DDR1	
1007_s_at	-1.8257200735147	0		PGM1	
201968_s_at	1.81818231032019	0			

AML MLL vs. T-ALL		samples: 15 / 9		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
242292_at	-3.53231266693437	0*	19.4	
243154_at	-3.1306973304726	0		
219891_at	3.05552709838153	0		FLJ20208
211404_s_at	2.9355923181049	0		APLP2
209499_x_at	2.75677919960856	0		TNFSF13
211495_x_at	2.73018317509301	0		TNFSF13
208702_x_at	2.59886997802643	0		APLP2
214875_x_at	2.52933264502392	0		APLP2
206111_at	2.43695278026584	0		RNASE2
209500_x_at	2.41035664982945	0		TNFSF13
210314_x_at	2.38921906328214	0		TNFSF13
225003_at	2.37212829914098	0		MBC3205
218122_s_at	-2.30056189156697	0		SENP2
204484_at	-2.28386643829897	0		PIK3C2B
205640_at	2.26383232065516	0		ALDH3B1
201105_at	2.26087708407154	0		LGALS1
200743_s_at	2.25956196871586	0		CLN2
222698_s_at	2.23788003936299	0		IMPACT
200742_s_at	2.2220970534291	0		CLN2
201537_s_at	2.16766347414866	0		DUSP3

AML MLL vs. AML +8		samples: 15 / 10		
accuracy	1			
confidence	0.8689072208975			
gene	signal-to-noise	p	decision limit	gene symbol
200056_s_at - HG-U133A	-1.60303643777462	0		C1D
212250_at	-1.47262825515036	0		
228024_at	-1.43968630786794	0		PAK1
205355_at	-1.39534301157978	0		ACADSB
225700_at	-1.39419450937928	0.01		
234726_s_at	1.36257922965513	0		
202619_s_at	-1.34323877280623	0		PLOD2
205453_at	-1.29520111839967	0		HOXB2
202823_at	-1.28255326311509	0		TCEB1
210749_x_at	-1.26893758929818	0		DDR1
227786_at	-1.24020773870069	0		TRAP25
212479_s_at	-1.23922427261637	0*	437.3	FLJ13910
219312_s_at	-1.21983738431424	0		RINZF
218172_s_at	-1.21403337241271	0*	285.95	PRO2577
200867_at	-1.2110165320696	0*	531	
202956_at	-1.21043821718202	0*	550.6	BIG1
213902_at	-1.19710457307816	0		ASAH
239597_at	1.19444081572455	0		
214789_x_at	-1.19367799101574	0		SRP46
AFFX-r2-Ec-bioD-3_at - HG-U133B	0.789398697044362	0		

AML MLL vs. AML complex		samples: 15 / 36			
accuracy	1				
confidence	0.928537448772464				
gene	signal-to-noise	p	decision limit	gene symbol	
228083_at	1.83691594955677	0			
201105_at	1.56013660814198	0		LGALS1	
201377_at	-1.5390279619994	0		KIAA0144	
201358_s_at	-1.46121373620596	0		COPB	
203387_s_at	-1.43200690176451	0		KIAA0603	
201585_s_at	-1.42612880048733	0		SFPQ	
222982_x_at	-1.4232823410753	0		SLC38A2	
202746_at	-1.40541613814493	0*	277.15		
204951_at	-1.38290450200254	0*	224.05	ARHH	
203725_at	-1.35090921185734	0		GADD45A	
203544_s_at	-1.33195316834084	0		STAM	
225804_at	1.3109814684568	0			
203386_at	-1.30903268579411	0		KIAA0603	
201359_at	-1.3066438308133	0		COPB	
201830_s_at	-1.29170882160348	0		NET1	
218041_x_at	-1.27263528593652	0		PRO1068	
223318_s_at	1.27042416454958	0		MGC10974	
212222_at	-1.26786775770503	0		KIAA0077	
201829_at	-1.26235979300155	0		NET1	
239647_at	1.09622576767215	0			

AML MLL vs. AML normal		samples: 15 / 62		
accuracy	0.948051948051948			
confidence	0.903617550418171			
failed:	3,4,72,76			
gene	signal-to-noise	p	decision limit	gene symbol
205453_at	-1.38558116676561	0*	203.25	HOXB2
222465_at	-1.29236441992376	0		C15orf15
225406_at	-1.29036630213613	0*	191.3	TSG
200829_x_at	-1.1349148684836	0		ZNF207
225326_at	-1.12776286034489	0		KIAA1311
200056_s_at - HG-U133B	-1.12696320763032	0		C1D
238856_s_at	-1.09612740485765	0		
227786_at	-1.08912698999125	0		TRAP25
200673_at	-1.08754065564232	0		LAPTM4A
226250_at	-1.08598948671591	0		
233559_s_at	1.08564709559314	0		FENS-1
228904_at	-1.07283266172579	0		
227680_at	-1.06344466244967	0		
223982_s_at	-1.06119523760418	0		IPLA2
202377_at	-1.05377199670316	0		HSOBRGRP
225700_at	-1.04818024157045	0		
209160_at	-1.04660040264575	0		AKR1C3
229232_at	-1.04476453216419	0		
231870_s_at	-1.04348230442961	0		LOC51068
201105_at	1.03632090944134	0		LGALS1

AML MLL vs. AML t(8;21)		samples: 15 / 13			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
214651_s_at	2.42114497347366	0	3881.25	HOXA9	
201105_at	2.17374439391796	0*		LGALS1	
228827_at	-2.03460798747208	0			
206009_at	-2.02655766969028	0		ITGA9	
228083_at	1.99768244710951	0			
213150_at	1.98436589229381	0		HOXA10	
50221_at	1.94810783752319	0			
221581_s_at	1.89677192380517	0		WBSCR5	
235753_at	1.88396584115232	0			
206622_at	-1.79659162526109	0		TRH	
209905_at	1.76718971964498	0		HOXA9	
204069_at	1.75588643276789	0		MEIS1	
209160_at	-1.75500319419551	0		AKR1C3	
235818_at	-1.70111545046162	0			
223498_at	1.67798456165549	0			
211404_s_at	1.67488607654784	0		APLP2	
209500_x_at	1.66210516483391	0		TNFSF13	
203949_at	-1.65967693892027	0		MPO	
214875_x_at	1.65852470588382	0		APLP2	
56256_at	1.09757984221605	0		LOC51092	

CLL vs. all other		samples: 32 / 237		
accuracy	0.996282527881041			
confidence	1			
failed:	11			
gene	signal-to-noise	p	decision limit	gene symbol
224838_at	2.72658457901213	0	630.55	
239287_at	2.21787255431445	0*		
223514_at	2.1294564890461	0		CARD11
44790_s_at	2.04322734300157	0		FLJ21562
212590_at	2.0395652222237	0		
223287_s_at	2.01927297186102	0		FOXP1
228390_at	2.01736536531344	0		
219471_at	2.0123024445387	0		FLJ21562
208456_s_at	2.00649246957273	0		RRAS2
243780_at	1.99741020732395	0		
201998_at	1.97818562004593	0		SIAT1
223391_at	1.97429784627482	0		LOC81537
208091_s_at	1.95442592300049	0		DKFZP564K0822
225927_at	1.94521013683932	0		MAP3K1
202589_at	-1.94332001129586	0		TYMS
229072_at	1.94278755168998	0		
229844_at	1.93701311168151	0		
214615_at	1.91900370555866	0		P2Y10
230768_at	1.89700621262016	0		
224837_at	1.88521474574714	0		FOXP1

CLL vs. CML

samples: 32 / 14

accuracy

1

confidence

1

gene

signal-to-noise

p

decision limit

gene symbol

210254_at

-4.88339464327865

0*

3718.45

205557_at

-4.67296996074416

0

BPI

206111_at

-4.55904506479679

0

RNASE2

209619_at

4.54717160557061

0

CD74

202503_s_at

-4.46030015155587

0

KIAA0101

206871_at

-4.43465869214911

0

ELA2

203949_at

-4.36878588501229

0

MPO

202589_at

-4.25959896335016

0

TYMS

212268_at

-4.11824280019806

0

SERPINB1

212531_at

-4.10884128760506

0

LCN2

206676_at

-3.98482491918087

0

CEACAM8

204670_x_at

3.97453356450998

0

HLA-DRB5

210334_x_at

-3.95114669210453

0

BIRC5

200654_at

-3.73551197850169

0

P4HB

208306_x_at

3.6021607716515

0

HLA-DRB4

224838_at

3.57587529198941

0

213572_s_at

-3.56773642902922

0

SERPINB1

207269_at

-3.5389139132598

0

DEFA4

212750_at

3.51249429987917

0

PPP1R16B

41577_at

3.13666804152596

0

PPP1R16B

CLL vs. normal BM

samples: 32 / 9

accuracy

1

confidence

1

gene	signal-to-noise	p	decision limit	gene symbol
204776_at	-4.80025506569938	0*	163.3	THBS4
210613_s_at	-4.76199342875923	0		SYNGR1
218662_s_at	-4.49242317171143	0		HCAP-G
202503_s_at	-4.2272639947421	0		KIAA0101
202580_x_at	-4.18939678293477	0		FOXN1
205051_s_at	-4.15661524563327	0		KIT
202018_s_at	-4.09501572722927	0		LTF
230988_at	-4.0486666186669	0		
206871_at	-4.04477996703664	0		ELA2
224975_at	-3.78270966714705	0		NFIA
227230_s_at	-3.69195069014622	0		KIAA1211
209714_s_at	-3.55884052493629	0		CDKN3
212531_at	-3.54256621978711	0		LCN2
214575_s_at	-3.53838586077798	0		AZU1
202589_at	-3.38277320357567	0		TYMS
223785_at	-3.37348567040386	0		FLJ10719
202705_at	-3.36111245088024	0		CCNB2
224976_at	-3.35971882977735	0		NFIA
210052_s_at	-3.33990497740824	0		C20orf1

CLL vs. ALL t(8;14)

samples: 32 / 4

accuracy

1

confidence

1

gene	signal-to-noise	p	decision limit	gene symbol
202580_x_at	-7.18159480292423	0*	218.2	FOXM1
209891_at	-6.98895220029526	0		AD024
227039_at	3.70691051731571	0		AKAP13
218663_at	-3.68808195572391	0		HCAP-G
36004_at	3.51464925040429	0		IKBKG
226936_at	-3.44796352148406	0		
228211_at	3.34271829518438	0		
218355_at	-3.32490989672808	0		KIF4A
201761_at	-3.28097759120759	0		MTHFD2
205837_s_at	-3.18161701452463	0		GYPA
210052_s_at	-3.16637659493241	0		C20orf1
202095_s_at	-3.11748537316183	0		BIRC5
202503_s_at	-3.09625623775405	0		KIAA0101
212020_s_at	-3.09152886109552	0		MKI67
216833_x_at	-3.08262837314566	0		
228361_at	-3.05435230901633	0		
212022_s_at	-3.01225907956052	0		MKI67
227065_at	3.00267996592052	0		COL5A2
218039_at	-2.9948995053224	0		ANKT
36920_at	2.10655917810938	0		MTM1

CLL vs. ALL B not Ph		samples: 32 / 9		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
225927_at	3.15130564055876	0*	1541.45	MAP3K1
213927_at	2.64985304902657	0		
201462_at	2.62143810029708	0		KIAA0193
224838_at	2.5941283416844	0		
213453_x_at	-2.18846578413759	0		GAPD
239287_at	2.18590081196116	0		
208091_s_at	2.12019333022318	0		DKFZP564K0822
201998_at	2.1165316341122	0		SIAT1
224848_at	-2.11049474415864	0		
202863_at	2.08665988043685	0		SP100
225592_at	-2.07634399767076	0		NRM
205805_s_at	2.04616469387812	0		ROR1
228390_at	2.03697588799482	0		
AFFX-				
HUMGAPDH/M33197_3_at	-			
HG-U133B	-2.02578116307399	0		GAPD
220768_s_at	2.01657972292803	0		CSNK1G3
221858_at	2.00702836396881	0		KIAA0608
214786_at	2.00594347120247	0		MAP3K1
224570_s_at	-2.00161337456916	0		
202625_at	1.99700437780915	0		LYN
AFFX-r2-Hs18SrRNA-3_s_at -				
HG-U133B	0.670536484443349	0		

CLL vs. ALL Ph		samples: 32 / 15		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
204663_at	-3.923285216392	0*	80.55	ME3
203373_at	-3.78247945374324	0		STAT12
225927_at	3.05858766321181	0		MAP3K1
223514_at	2.79698500849851	0		CARD11
210487_at	-2.66400596339357	0		DNTT
213927_at	2.64985304902657	0		
237337_at	2.52705433891484	0		
236280_at	2.49746424904494	0		
227900_at	2.49040043479395	0		
211709_s_at	-2.45092080989795	0		SCGF
224833_at	2.40705165058966	0		ETS1
226545_at	-2.40457551567713	0		
208091_s_at	2.38274758846201	0		DKFZP564K0822
235674_at	2.37963455734461	0		
234107_s_at	2.36302665773918	0		
223462_at	2.32337125093609	0		MGC4618
201462_at	2.3212369641096	0		KIAA0193
223391_at	2.30224083750022	0		LOC81537
212719_at	-2.29194173393375	0		SCOP

CLL vs. T-ALL		samples: 32 / 9		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
201417_at	-3.83747798152129	0*	2230.95	
201416_at	-3.69716215884899	0		SOX4
221858_at	2.73818494452306	0		KIAA0608
213772_s_at	2.72201152228286	0		GGA2
224932_at	2.6366912338985	0		PRSS2
224847_at	-2.63602874545103	0		
201462_at	2.62143810029708	0		KIAA0193
224848_at	-2.60776696130397	0		
243780_at	2.49991585531364	0		
227900_at	2.49040043479395	0		
202625_at	2.4377901797746	0		LYN
228390_at	2.41659743191322	0		
201998_at	2.39630335572289	0		SIAT1
226545_at	-2.3815195487075	0		
204446_s_at	2.37716091038765	0		ALOX5
204192_at	2.34749349754959	0		CD37
219076_s_at	-2.31227318629435	0		PXMP2
206398_s_at	2.30227312148638	0		CD19
224838_at	2.29208011575118	0		
212827_at	2.28758794629918	0		IGHM

CLL vs. AML +8

samples: 32 / 10

accuracy

1

confidence

1

gene	signal-to-noise	p	decision limit	gene symbol
224838_at	3.16933404672116	0		
223514_at	2.79698500849851	0		CARD11
212827_at	2.5676577800083	0		IGHM
201200_at	-2.5208800664045	0		CREG
242633_x_at	2.38085767453167	0		
208456_s_at	2.34106774724323	0		RRAS2
212590_at	2.3295599530646	0		
44790_s_at	2.32854069014676	0		FLJ21562
219471_at	2.27189811261511	0		FLJ21562
202441_at	-2.26915475899159	0		KEO4
209374_s_at	2.26352755463127	0		IGHM
243780_at	2.25989352775893	0		
204215_at	2.24311505389492	0*	906.65	MGC4175
223382_s_at	-2.21844659554677	0		NIN283
201163_s_at	-2.2061831531108	0		IGFBP7
224837_at	2.17714293481922	0		FOXP1
223391_at	2.1733535915887	0		LOC81537
208091_s_at	2.17150813050761	0		DKFZP564K0822
205933_at	2.16573909337041	0		SETBP1
239287_at	2.1598880074389	0		

CLL vs. AML complex		samples: 32 / 36		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
224838_at	2.78969388721613	0		
235674_at	2.37963455734461	0		
243780_at	2.32051881321218	0		
239287_at	2.24074490580899	0		
223514_at	2.18755403591948	0		CARD11
222680_s_at	-2.18354473266858	0*	203.95	RAMP
209619_at	2.13206191976271	0		CD74
202503_s_at	-2.11188972263141	0		KIAA0101
208456_s_at	2.10620770802115	0		RRAS2
208864_s_at	-2.10162761752294	0		TXN
212590_at	2.09310293747601	0		
201200_at	-2.05492899324696	0		CREG
212827_at	2.05442625446282	0		IGHM
224837_at	2.04951179193956	0		FOXP1
205805_s_at	2.04616469387812	0		ROR1
244261_at	2.03144018714413	0		
223287_s_at	2.0252763158281	0		FOXP1
208091_s_at	2.0139098675012	0		DKFZP564K0822
226989_at	2.00631003964875	0		
236854_at	1.99292097643003	0		

CLL vs. AML normal	samples: 32 / 62			
accuracy	0.98936170212766			
confidence	1			
failed:	11			
gene	signal-to-noise	p	decision limit	gene symbol
224838_at	2.80936017892095	0*	2987.7	
243780_at	2.42900650257202	0		
223514_at	2.40431982389629	0		CARD11
201200_at	-2.28363968538296	0		CREG
201998_at	2.19987941765164	0		SIAT1
44790_s_at	2.18842053042545	0		FLJ21562
205049_s_at	2.18662155440889	0		CD79A
239287_at	2.17948863877979	0		
223287_s_at	2.16628667951355	0		FOXP1
223391_at	2.16298199717166	0		LOC81537
219471_at	2.13618332752253	0		FLJ21562
225175_s_at	2.12811708839772	0		CTL2
204215_at	2.11642877909845	0		MGC4175
236280_at	2.11271003733104	0		
208456_s_at	2.10890038745727	0		RRAS2
206398_s_at	2.09984081904119	0		CD19
212827_at	2.09850222830603	0		IGHM
228390_at	2.09600254213173	0		
229072_at	2.09351406943008	0		
214615_at	2.06329249104139	0		P2Y10

CLL vs. AML t(8;21)		samples: 32 / 13		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
203949_at	-3.50330789770673	0		MPO
224838_at	3.25663434332492	0		
205192_at	3.21758439151756	0*	113.25	MAP3K14
211709_s_at	-2.95109939287116	0		SCGF
212827_at	2.84469338495376	0		IGHM
230768_at	2.8154401362934	0		
206009_at	-2.7972720292112	0		ITGA9
208091_s_at	2.63085873400942	0		DKFZP564K0822
208456_s_at	2.62810675193075	0		RRAS2
215215_s_at	-2.60039836996497	0		
203948_s_at	-2.56960807932381	0		MPO
201811_x_at	2.56895859687937	0		SH3BP5
243780_at	2.51082778037667	0		
212590_at	2.50058834205242	0		
227900_at	2.49040043479395	0		
226546_at	-2.44432895386159	0		
225927_at	2.44085004959256	0		MAP3K1
212589_at	2.43561411833392	0		RRAS2
228390_at	2.41659743191322	0		
225246_at	2.39661265710521	0		STIM2

CML vs. all other	samples: 14 / 255			
accuracy	0.981412639405205			
confidence	0.984251851969928			
failed:	4,6,10,14,115			
gene	signal-to-noise	p	decision limit	gene symbol
212531_at	2.20686225450673	0		LCN2
205557_at	2.19817622063178	0*	11581.65	BPI
206676_at	2.01751329912518	0		CEACAM8
209772_s_at	1.89825970350824	0*	3429.4	CD24
207802_at	1.84335905687648	0		SGP28
216379_x_at	1.76253321043545	0		
209771_x_at	1.75699226119665	0		CD24
203936_s_at	1.75554347155831	0		MMP9
211657_at	1.69149085236384	0		
203757_s_at	1.6780512743379	0		CEACAM6
210254_at	1.6590320804534	0		
202018_s_at	1.64680728641866	0		LTF
211275_s_at	1.62477051547664	0		GYG
205513_at	1.60415014432038	0		TCN1
205863_at	1.60339454990244	0		S100A12
223839_s_at	1.57424844312026	0		
210244_at	1.56058501019954	0		CAMP
206440_at	1.5590538838617	0		VELI1
207269_at	1.55083422089021	0		DEFA4
204174_at	1.53747851176966	0		ALOX5AP

CML vs. normal BM		samples: 14 / 9		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
227198_at	-3.96995770729437	0*	39.95	
204562_at	-3.83910818190111	0		IRF4
227749_at	-3.11980636745679	0		
228377_at	-2.65145492785893	0		KIAA1384
226713_at	-2.28229285614419	0		
209619_at	-2.27384420268273	0		CD74
227375_at	-2.22184735546056	0		DKFZP566D1346
204057_at	-2.13119125485664	0		ICSBP1
201506_at	-2.05058862618543	0		TGFB1
221558_s_at	-2.0055054625083	0		LEF1
227867_at	-2.00414646646454	0		
225331_at	-1.95134035825926	0		
223280_x_at	-1.95125537387335	0		MS4A6A
243780_at	-1.94601159348593	0		
228055_at	-1.94418493221925	0		
204670_x_at	-1.94197079510435	0		HLA-DRB5
208683_at	-1.93662356244796	0		CAPN2
210356_x_at	-1.92014292171279	0		MS4A2
209670_at	-1.89146017871026	0		TRA
AFFX-				
HUMGAPDH/M33197_3_at				
HG-U133B	1.0887744230798	0		GAPD

CML vs. ALL t(8;14)		samples: 14 / 4		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
231215_at	-3.69904177219169	0*	17.25	
212400_at	-3.60679086659289	0		
239835_at	-3.24273732421016	0		KIAA1842
214439_x_at	-3.01379256143662	0		BIN1
227173_s_at	-2.97620214103741	0		BACH2
209619_at	-2.86528990843459	0		CD74
234660_s_at	-2.81161728678359	0		DIS3
202723_s_at	-2.69572816449622	0		FOXO1A
227700_x_at	-2.59859831428636	0		FLJ10709
219202_at	-2.52442131777509	0		FLJ22341
204638_at	-2.51835721417786	0		ACP5
222147_s_at	-2.47042047428454	0		
213772_s_at	-2.41552637854988	0		GGA2
203932_at	-2.39804753895984	0		HLA-DMB
205145_s_at	-2.34102992713809	0		MYL5
221969_at	-2.278395672233	0.01		PAX5
217521_at	2.26710710056045	0		
205541_s_at	-2.22303735713359	0		GSPT2
204661_at	-2.15814023268535	0		CDW52
242729_at	2.02602724250151	0		

CML vs. ALL B not Ph		samples: 14 / 9		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
206440_at	3.54851691296324	0*	69.75	VELL1
223839_s_at	2.95162251991881	0		
201482_at	2.5967465282815	0		QSCN6
223246_s_at	-2.53289104519377	0		STRBP
202477_s_at	-2.36949525800043	0		GCP2
227415_at	-2.35663515228965	0		
202819_s_at	-2.31208048847973	0		TCEB3
226876_at	2.29929647597952	0		
200654_at	2.2916645921996	0		P4HB
231472_at	-2.27133126588153	0		
217521_at	2.26710710056045	0		
218764_at	-2.26149206068996	0		MGC5363
219615_s_at	2.21717677908473	0		KCNK5
219111_s_at	-2.20588673666352	0		MGC2835
212268_at	2.20005764504112	0		SERPINB1
211275_s_at	2.1595066613388	0		GYG
211990_at	-2.15004013194548	0		HLA-DPA1
206676_at	2.13116752502457	0		CEACAM8
235818_at	2.13111499669481	0		
210254_at	2.07581294141343	0		

CML vs. ALL Ph		samples: 14 / 15		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
209619_at	-3.47132181247921	0*	5777.85	CD74
212778_at	-3.09966497846595	0		KIAA0602
201029_s_at	-3.08460906542498	0		MIC2
214317_x_at	-3.02953000176234	0		RPS9
202332_at	-2.9539112535883	0		CSNK1E
211990_at	-2.80086525597245	0		HLA-DPA1
203373_at	-2.76056827822619	0		STAT12
210487_at	-2.66400596339357	0		DNTT
226844_at	-2.53578669067924	0		
207971_s_at	-2.4877090389281	0		KIAA0582
206440_at	2.45272667930868	0		VELI1
205513_at	2.38968722893052	0		TCN1
211275_s_at	2.33552678870234	0		GYG
204670_x_at	-2.32905695313267	0		HLA-DRB5
205557_at	2.3286749741246	0		BPI
220000_at	2.32132983989275	0		SIGLEC5
212531_at	2.31169568945083	0		LCN2
204174_at	2.3066969794321	0		ALOX5AP
225386_s_at	2.25229241478444	0		LOC92906
206111_at	2.22277368410809	0		RNASE2

CML vs. T-ALL

samples: 14 / 9

accuracy

1

confidence

1

gene**signal-to-noise****p****decision limit****gene symbol**

210254_at

4.72390509810889

0*

3562.85

206111_at

4.12411957901486

0

RNASE2

205557_at

4.12268252311326

0

BPI

216379_x_at

4.09576684675689

0

209771_x_at

4.04268115620178

0

CD24

204484_at

-3.92079658637056

0

PIK3C2B

203949_at

3.82080923209307

0

MPO

206871_at

3.79666500221894

0

ELA2

212268_at

3.66762573362107

0

SERPINB1

239071_at

-3.65785660037409

0

209772_s_at

3.61720812003475

0

CD24

212531_at

3.55056769994448

0

LCN2

206440_at

3.54851691296324

0

VELI1

242292_at

-3.53231266693437

0

206676_at

3.51041964854693

0

CEACAM8

218224_at

-3.28568428621792

0

PNMA1

211657_at

3.27814094785335

0

231215_at

-3.27770330337019

0

211275_s_at

3.26113496045954

0

GYG

203757_s_at

3.16440848129156

0

CEACAM6

CML vs. AML +8	samples: 14 / 10			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
212531_at	3.91758233758871	0*	6654.5	LCN2
218151_x_at	-3.61342068798238	0		FLJ11856
203188_at	-2.49453997369644	0		B3GNT6
225014_at	-2.46286744087574	0		
223894_s_at	2.42404553998791	0		FTS
227999_at	-2.41422896946156	0		LOC170394
210244_at	2.30650676975445	0		CAMP
223226_x_at	-2.1556086960975	0		MGC3181
205849_s_at	-2.15471806280279	0		UQCRB
203936_s_at	2.12656987689311	0		MMP9
202080_s_at	-2.08086044698338	0		KIAA1042
212146_at	-2.00720003739628	0		KIAA0842
210749_x_at	-2.00702022115248	0		DDR1
220755_s_at	-1.97451125809376	0		
211743_s_at	1.88718047009153	0		PRG2
214317_x_at	-1.86316203101213	0		RPS9
214475_x_at	1.8601686492104	0		CAPN3
200094_s_at - HG-U133A	-1.83127854302456	0		EEF2
223939_at	1.81572736683912	0		GPR91
229934_at	1.65483415989943	0		

CML vs. AML complex

samples: 14 / 36

accuracy

0.98

confidence

1

failed:

19

gene	signal-to-noise	p	decision limit	gene symbol
209772_s_at	2.25515756155772	0	10028.8	CD24
212531_at	2.16780856655461	0*		LCN2
210244_at	2.05958595591104	0		CAMP
205557_at	1.88114022725824	0		BPI
207802_at	1.84224616530014	0		SGP28
203936_s_at	1.83245146841284	0		MMP9
206676_at	1.82688412686061	0		CEACAM8
216379_x_at	1.82175067686641	0		
209771_x_at	1.71430561727442	0		CD24
202265_at	-1.71011447772371	0		BMI1
209186_at	-1.65481819707492	0		ATP2A2
201029_s_at	-1.6407978740451	0		MIC2
206440_at	1.62023824679434	0		VELL1
218144_s_at	-1.60220955278722	0		FLJ22056
212783_at	-1.60173956589805	0		DKFZp761B2423
225065_x_at	1.5634162479603	0		
214317_x_at	-1.51909514839257	0		RPS9
212232_at	-1.51499149327941	0		KIAA1014
223894_s_at	1.50378092313755	0		FTS
207269_at	1.49292374711871	0		DEFA4

CML vs. AML normal	samples: 14 / 62			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
212531_at	3.52937454592387	0*	9007.35	LCN2
209772_s_at	2.62224687740926	0		CD24
207802_at	2.60464949585023	0		SGP28
205557_at	2.59981269961356	0		BPI
206676_at	2.51996784029752	0		CEACAM8
205513_at	2.39713364221477	0		TCN1
209771_x_at	2.3694290541236	0		CD24
216379_x_at	2.36313392615064	0		
211657_at	2.35374478763084	0		
203757_s_at	2.29281876629007	0		CEACAM6
202018_s_at	2.19711362051377	0		LTF
210254_at	2.16927497946765	0		
203021_at	2.12970551783084	0		SLPI
205863_at	2.10812748771569	0		S100A12
203936_s_at	2.07272259731953	0		MMP9
210244_at	2.03624546792529	0		CAMP
204351_at	2.0071543551955	0		S100P
211275_s_at	1.97937290056753	0		GYG
224967_at	1.96229148265436	0		
223894_s_at	1.92953251923329	0		FTS

CML vs. AML t(8;21)

samples: 14 / 13

accuracy

1

confidence

1

gene	signal-to-noise	p	decision limit	gene symbol
207802_at	2.83774385104531	0		SGP28
201425_at	2.50825834074572	0		ALDH2
201029_s_at	-2.22223571455337	0*	3078.2	MIC2
205653_at	2.20106889451589	0		CTSG
202391_at	2.10168460148023	0		BASP1
209619_at	-2.0547003400447	0		CD74
228827_at	-2.03460798747208	0		
204670_x_at	-1.98893997185408	0		HLA-DRB5
212531_at	1.96994267101106	0		LCN2
203936_s_at	1.92996861752981	0		MMP9
225386_s_at	1.90963950502737	0		LOC92906
226878_at	-1.90647418854412	0		
201015_s_at	-1.90408812555782	0		JUP
201281_at	-1.88812152152812	0		ADRM1
210982_s_at	-1.87330616648773	0		HLA-DRA
210254_at	1.87025014628174	0		
201137_s_at	-1.84763478416102	0		HLA-DPB1
202545_at	1.81501795739179	0		PRKCD
228485_s_at	1.81223837093458	0		CDW92
231969_at	1.61927333154015	0		DKFZp762K222

normal BM vs. all other	samples: 9 / 260			
accuracy	0.970260223048327			
confidence	1			
failed:	1,3,4,5,7,8,9,234			
gene	signal-to-noise	p	decision limit	gene symbol
202018_s_at	1.70014923965644	0		LTF
231241_at	1.68875870396623	0		
212531_at	1.61671894194992	0		LCN2
210244_at	1.4725412229519	0		CAMP
244652_at	1.41007652726897	0		
218916_at	-1.40959768522889	0		FLJ23436
208141_s_at	-1.39496085050899	0		MGC4293
218516_s_at	-1.39489208362807	0		FLJ20421
224976_at	1.38035857849962	0		NFIA
201396_s_at	-1.35501592670165	0		SGT
230988_at	1.27806474591682	0		
200631_s_at	-1.27257367942543	0		SET
224975_at	1.25475272090295	0		NFIA
203535_at	1.24698765220296	0		S100A9
227497_at	1.24053728574653	0*	317.95	
225792_at	1.2371690464102	0		
203367_at	-1.23177778244874	0		DUSP14
40189_at	-1.22367056036721	0		SET
225700_at	1.22315772266762	0		
223785_at	1.22097206282821	0		FLJ10719

normal BM vs. ALL t(8;14)		samples: 9 / 4			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
222147_s_at	-5.80632286389653	0*	48.2		
209380_s_at	4.30105342509009	0		ABCC5	
230988_at	4.0486666186669	0			
227230_s_at	3.69195069014622	0		KIAA1211	
201278_at	3.59730622800604	0		DAB2	
205051_s_at	3.55673529468534	0		KIT	
214558_at	3.49255759470258	0		GPR12	
201988_s_at	3.46251302734757	0		CREBL2	
223253_at	3.45322097101822	0		UCC1	
204285_s_at	-3.35570555370453	0		PMAIP1	
237006_at	3.14219078440997	0			
217047_s_at	3.00448756016945	0			
243020_at	2.97861252444615	0			
205690_s_at	-2.97763156027721	0		G10	
234764_x_at	2.9597816169315	0			
209160_at	2.88288854646291	0.01		AKR1C3	
239835_at	-2.82125904680112	0		KIAA1842	
242434_at	-2.60351764410894	0.01			
228708_at	2.60104548908002	0.01			
229575_at	2.59826531472399	0			

normal BM vs. ALL B not Ph		samples: 9 / 9		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
201506_at	3.72288560994884	0*	464.35	TGFB1
218718_at	3.24294310152425	0		PDGFC
205051_s_at	3.03451031560789	0		KIT
235818_at	2.5546546541523	0		
202382_s_at	2.39296453276424	0		GNPI
221802_s_at	2.32414568373485	0		KIAA1598
238066_at	2.17647785634866	0		RBP7
203645_s_at	2.13814112768782	0		CD163
227038_at	2.09057615422001	0		
225792_at	2.07680085776485	0		
202729_s_at	2.04654552970378	0		LTBP1
230441_at	-2.03717805375485	0		
212989_at	2.00592033097705	0		
201462_at	1.98840399134665	0		KIAA0193
227627_at	1.97570787395888	0		SGKL
204112_s_at	1.90974025156521	0		HNMT
204285_s_at	-1.90604496284052	0		PMAIP1
223044_at	1.88064158446644	0		SLC11A3
223839_s_at	1.86406616667336	0		
204225_at	1.85888952621093	0		HDAC4

normal BM vs. ALL Ph		samples: 9 / 15		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
225792_at	5.04037264761662	0*	76.45	
224976_at	4.534006778733	0		NFIA
227230_s_at	3.69195069014622	0		KIAA1211
203373_at	-3.60116056485263	0		STAT12
202332_at	-3.19705046805115	0		CSNK1E
212778_at	-3.09966497846595	0		KIAA0602
230988_at	3.03359562676407	0		
218718_at	3.0129378014466	0		PDGFC
205624_at	2.79751505147013	0		CPA3
224975_at	2.78377945957649	0		NFIA
234107_s_at	2.7482082597836	0		
217988_at	-2.7439427550045	0		HEI10
202945_at	-2.67000372671022	0		FPGS
218916_at	-2.6636521234692	0		FLJ23436
223044_at	2.59882500535427	0		SLC11A3
226751_at	2.41273912703748	0		DKFZP566K1924
210487_at	-2.38376037071424	0		DNTT
201029_s_at	-2.37712949687212	0		MIC2
207971_s_at	-2.36738543730614	0		KIAA0582
203645_s_at	2.32470988727879	0		CD163

normal BM vs. T-ALL		samples: 9 / 9		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
231241_at	5.25713497545753	0*	52.3	
225792_at	5.04037264761662	0		
224976_at	4.534006778733	0		NFIA
204484_at	-3.92079658637056	0		PIK3C2B
218516_s_at	-3.89821124480393	0.01		FLJ20421
244652_at	3.8571916430704	0		
210613_s_at	3.6441364713354	0		SYNGR1
206488_s_at	3.59792987181253	0		CD36
201416_at	-3.57631738716755	0		SOX4
201417_at	-3.57222567838335	0		
218224_at	-3.56533208466192	0		PNMA1
206871_at	3.49320660549908	0		ELA2
214575_s_at	3.38517251606938	0		AZU1
221188_s_at	3.26852421442154	0		CIDEB
203104_at	3.11161266045758	0		CSF1R
226190_at	3.08925054797494	0		
202018_s_at	3.06471974822162	0		LTF
200631_s_at	-3.05905666007645	0		SET
224970_at	3.05809311507561	0		NFIA
212531_at	3.03461908631694	0		LCN2

normal BM vs. AML +8		samples: 9 / 10			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
231241_at	5.25713497545753	0*	52.3		
218916_at	-4.40926777727725	0		FLJ23436	
218151_x_at	-3.61342068798238	0		FLJ11856	
212531_at	3.35638912536087	0		LCN2	
225014_at	-2.46286744087574	0			
210244_at	2.4347108722936	0		CAMP	
227999_at	-2.41422896946156	0		LOC170394	
220755_s_at	-2.40201593179233	0			
202945_at	-2.37212917164108	0		FPGS	
214109_at	2.28939588941522	0		LRBA	
225792_at	2.20832306168575	0			
238066_at	2.17647785634866	0		RBP7	
217179_x_at	2.173252865121	0			
200631_s_at	-2.1126574466818	0		SET	
234764_x_at	2.11173306630787	0			
225547_at	-2.10764119746987	0			
205849_s_at	-2.04438654979845	0		UQCRB	
208141_s_at	-2.04344739454244	0		MGC4293	
233613_x_at	2.02519262390017	0			

normal BM vs. AML complex		samples: 9 / 36		
accuracy	0.9777777777777778			
confidence	1			
failed:	15			
gene	signal-to-noise	p	decision limit	gene symbol
231241_at	2.20113810647196	0*	94.5	
210244_at	2.15797898100991	0		CAMP
226734_at	2.10647394623844	0		
218516_s_at	-2.0003648205556	0		FLJ20421
244652_at	1.9350839662771	0		
201595_s_at	-1.81799799553143	0		HT010
212531_at	1.80637620431712	0		LCN2
201396_s_at	-1.79606593499252	0		SGT
203092_at	-1.77664454556306	0		TIMM44
230795_at	-1.75873906279717	0		H4F2
228377_at	1.70396224015785	0		KIAA1384
208141_s_at	-1.66429492261381	0		MGC4293
202265_at	-1.62376492554641	0		BMI1
202018_s_at	1.60476985758804	0		LTF
218916_at	-1.58708293547372	0		FLJ23436
224406_s_at	1.57633156642315	0		IRTA2
209806_at	-1.57424329592102	0		H2B/S
208645_s_at	1.5695109709269	0		
200040_at - HG-U133A	-1.548128254162	0		KHDRBS1
AFFX-HSAC07/X00351_M_at -				
HG-U133A	1.11476993738169	0		ACTB

normal BM vs. AML normal	samples: 9 / 62			
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
212531_at	3.03296310695958	0*	8390.45	LCN2
202018_s_at	2.55569861815605	0		LTF
210244_at	2.12911144557531	0		CAMP
231241_at	1.90756814920388	0		
234764_x_at	1.88445719282136	0		
238066_at	1.84490304262637	0		RBP7
218516_s_at	-1.76767038599239	0		FLJ20421
214651_s_at	-1.75409579509524	0		HOXA9
207802_at	1.69982859144728	0		SGP28
203535_at	1.6861966835666	0		S100A9
224976_at	1.68580070345942	0		NFIA
235818_at	1.65829753113564	0		
226188_at	1.63500287325021	0		
208651_x_at	1.6330531805719	0		CD24
214523_at	1.61056786968333	0		CEBPE
206871_at	1.60161598002874	0		ELA2
224970_at	1.57809657249869	0		NFIA
210004_at	1.57705611671231	0		OLR1
208141_s_at	-1.55515435811455	0		MGC4293
215379_x_at	1.53008885935316	0		IGLJ3

normal BM vs. AML t{8;21)		samples: 9 / 13		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
225792_at	5.04037264761662	0*	76.45	
224976_at	4.534006778733	0		NFIA
201425_at	3.96306688659586	0		ALDH2
201506_at	3.72288560994884	0		TGFB1
208146_s_at	3.28524851571637	0		CPVL
224970_at	3.05809311507561	0		NFIA
206488_s_at	2.8751017477522	0		CD36
226818_at	2.67802773991406	0		
224975_at	2.55138740597295	0		NFIA
227388_at	2.49815087819486	0		
217963_s_at	2.48471435523086	0		HCS
233613_x_at	2.45189729191801	0		
228766_at	2.45082385023982	0		
208908_s_at	2.41879730006023	0		CAST
212586_at	2.33228373164484	0		ARTS-1
221802_s_at	2.32414568373485	0		KIAA1598
224823_at	2.30113027005505	0		
213624_at	2.29634946162627	0		ASM3A
221731_x_at	2.26796857130761	0		CSPG2
225426_at	2.26611296861875	0		

ALL t(8;14) vs. ALL Ph

samples: 4 / 15

accuracy

1

confidence

1

gene	signal-to-noise	p	decision limit	gene symbol
204663_at	-3.923285216392	0*	80.55	ME3
203373_at	-3.79361888147031	0		STAT2
207971_s_at	-3.75632756767036	0		KIAA0582
221834_at	-3.73210732395713	0		
212535_at	-3.35180803492209	0		
210487_at	-2.66400596339357	0		DNTT
226607_at	-2.65303285070543	0		L3MBTL
214505_s_at	-2.30002142127038	0		FHL1
226545_at	-2.26350222846019	0		
201540_at	-2.21889045310099	0		FHL1
209253_at	-2.17983750831107	0		SCAM-1
228496_s_at	-2.17784383479245	0		CRIM1
213854_at	-2.14963630962421	0		SYNGR1
228211_at	-2.14770747938169	0		
212012_at	-2.10857376713896	0		D2S448
208217_at	-2.10769716540219	0		GABRR2
202519_at	-2.0579870997007	0		MONDOA
218836_at	2.05747195088222	0		FLJ22638
211031_s_at	-2.05686503189171	0		CYLN2
50277_at	1.4804958933411	0		GGA1

ALL t(8;14) vs. T-ALL		samples: 4 / 9			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
213772_s_at	4.99941703918842	0*	105.35	GGA2	
236019_at	-4.8835710129593	0			
225277_at	-4.63399536600695	0			
40148_at	3.56542456382539	0		APBB2	
228211_at	-3.35861431980337	0			
201334_s_at	3.32612092220108	0		ARHGEF12	
201417_at	-2.74359054965603	0			
206241_at	-2.66958809534806	0		KPNA5	
208918_s_at	2.59071326340578	0		FLJ13052	
210038_at	-2.55792113825771	0			
225735_at	-2.54773299400117	0			
209253_at	-2.33749346955264	0		SCAM-1	
202262_x_at	-2.29867528817227	0		DDAH2	
225129_at	2.29232308514395	0		MDS026	
221969_at	2.278395672233	0		PAX5	
225080_at	2.24115131588386	0		MYO1C	
218338_at	-2.22116851483018	0		EDR1	
208664_s_at	-2.20362132175544	0		TTC3	
201029_s_at	-2.14618908100153	0.01		MIC2	
56256_at	1.43796973813133	0		LOC51092	

ALL t(8;14) vs. AML +8

samples: 4 / 10

accuracy

1

confidence

1

gene	signal-to-noise	p	decision limit	gene symbol
213159_at	-4.39324002240111	0*	42.05	KIAA0805
226607_at	-4.38967336864894	0		L3MBTL
205420_at	-3.4525752660757	0		PEX7
202137_s_at	-3.07008892450809	0		BS69
36004_at	-2.57531929513625	0.01		IKBKG
203731_s_at	-2.45523698701432	0		ZFP95
212349_at	-2.36608074328153	0		POFUT1
209253_at	-2.32838757070082	0.01		SCAM-1
213238_at	-2.28171034767303	0		ATP10D
223382_s_at	-2.21844659554677	0		NIN283
219291_at	-2.18210292149327	0		MDS009
212293_at	-2.11981778828952	0		KIAA0630
1729_at	-1.99780531744703	0		TRADD
225959_s_at	-1.99555471271853	0.01		NIN283
205690_s_at	1.97864646284407	0		G10
243579_at	1.96429396023857	0		MSI2
220564_at	1.95122068807877	0		FLJ11218
210896_s_at	-1.94074678448131	0		ASPH
221617_at	-1.92262620134603	0.02		

ALL t(8;14) vs. AML complex		samples: 4 / 36			
accuracy	0.975				
confidence	0.967090153309866				
failed:	4				
gene	signal-to-noise	p	decision limit	gene symbol	
36004_at	-1.99819054416994	0		IKBKG	
228410_at	-1.91203372111762	0		GAB3	
226291_at	-1.85352930781754	0		ALS2	
239478_x_at	-1.83892006057297	0			
201278_at	-1.78640641972044	0		DAB2	
213073_at	-1.78527733316412	0		KIAA0321	
36920_at	-1.77637196930535	0		MTM1	
237864_at	-1.75181406771053	0			
206550_s_at	-1.74071643864686	0.01		NUP155	
213779_at	-1.71354352282537	0			
237006_at	-1.71319042514024	0			
206847_s_at	-1.68023930751716	0		HOXA7	
213639_s_at	-1.6794904444526	0		KIAA0557	
40148_at	1.6627909781575	0*	64	APBB2	
210358_x_at	-1.62491966279342	0		MGC2306	
205420_at	-1.62469403094415	0		PEX7	
226499_at	-1.60847740357238	0			
212293_at	-1.56783564141892	0*	524.25	KIAA0630	
228211_at	-1.5662932955074	0			
AFFX-r2-Hs28SrRNA-5_at					
HG-U133B	0.804899059460234	0			

ALL t(8;14) vs. AML normal		samples: 4 / 62			
accuracy	1				
confidence	0.94492014468957				
gene	signal-to-noise	p	decision limit	gene symbol	
242774_at	2.1771591988175	0		SYNE-2	
226066_at	-2.1383489258559	0			
239478_x_at	-1.86376314754514	0			
40148_at	1.78834322080621	0*	53.3	APBB2	
214651_s_at	-1.72987407199338	0		HOXA9	
241421_at	-1.69137753712694	0			
225277_at	-1.68295316743627	0			
237864_at	-1.66733222775185	0			
231181_at	1.63598703935064	0			
227173_s_at	1.58512628703822	0		BACH2	
228410_at	-1.58118628637501	0		GAB3	
226607_at	-1.56767039969117	0		L3MBTL	
206398_s_at	1.56041095418581	0		CD19	
226590_at	-1.55939441513481	0.01			
223391_at	1.54577336325056	0		LOC81537	
205420_at	-1.53228798256568	0		PEX7	
240106_at	-1.53045374201368	0			
236019_at	-1.50700230486984	0			
214558_at	-1.50544788292166	0		GPR12	
AFFX-HUMRGE/M10098_3_at					
- HG-U133B	0.698344697289208	0			

ALL t(8;14) vs. AML t(8;21)		samples: 4 / 13			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
40148_at	3.56542456382539	0*	32.75	APBB2	
239835_at	3.10722969539603	0		KIAA1842	
225277_at	-2.97531197185908	0			
225306_s_at	-2.20761036808439	0			
210664_s_at	-2.19905382124823	0		TFPI	
218319_at	2.13133938217549	0		PEL1	
212985_at	2.10403815234864	0			
238155_at	2.09456306072679	0			
221617_at	-2.04115820286726	0			
220307_at	-2.04090815318901	0		CD244	
225250_at	2.04032419238326	0		STIM2	
217080_s_at	-2.03866301670049	0		HOMER-2B	
228827_at	-2.03460798747208	0			
214558_at	-2.02268322634707	0.01		GPR12	
230650_at	-2.02205697080977	0			
226546_at	-2.00802538838226	0			
219478_at	-1.99876002437156	0		WFDC1	
211709_s_at	-1.99340446769437	0		SCGF	
219789_at	-1.96292007200438	0		NPR3	
231181_at	1.9495774287402	0			

ALL B not Ph vs. all other

samples: 9 / 260

accuracy 0.988847583643123

confidence 0.749589637027985

failed: 1,2,8

gene	signal-to-noise	p	decision limit	gene symbol
230441_at	1.31003692018591	0		
202382_s_at	-1.16916758328947	0		GNPI
229253_at	-1.06515235605176	0		CTMP
201482_at	-1.03614111933273	0		QSCN6
214116_at	-1.00681323467099	0		BTD
224435_at	0.992700829908313	0		MGC4248
229344_x_at	0.972107787450054	0		KIAA1238
229487_at	0.965321723620396	0*	1	
217559_at	0.963455203763842	0		RPL10L
212592_at	0.956367645094086	0*	4436.6	
209197_at	0.921039694411825	0*	637.1	KIAA0080
223469_at	-0.914920276631408	0*	1	MGC10812
224739_at	0.904429749740017	0*	1	MG61
218351_at	-0.898398261455524	0*	145.5	FLJ20502
220744_s_at	-0.893719737391747	0*	1	WDR10
213582_at	-0.888860830483358	0*	1	ATP11A
219615_s_at	-0.8878326695192	0*	1	KCNK5
203795_s_at	0.880543704938786	0		BCL7A
229817_at	0.879488726239199	0		DKFZP434M098
244876_at	0.877426806604064	0		

ALL B not Ph vs. ALL Ph

samples: 9 / 15

accuracy 0.916666666666667

confidence 1

failed: 3,10

gene	signal-to-noise	p	decision limit	gene symbol
219358_s_at	-1.52735607926994	0		CENTA2
241383_at	-1.07499870203752	0.01		
213895_at	-1.05505220750298	0		EMP1
202123_s_at	-1.02481061931947	0*	753.7	ABL1
205911_at	-1.0236634987836	0		PTHR1
242223_at	1.02343172223498	0.01		
211709_s_at	-1.01491744255679	0		SCGF
234839_at	-1.00185285072786	0		
212150_at	-0.996731200580515	0		KIAA0143
221991_at	-0.987741661696868	0		NXPH3
218543_s_at	0.973909033712243	0		FLJ22693
201874_at	0.966766364385792	0		FLJ21047
212188_at	-0.947998533949464	0		LOC115207
241810_at	-0.944344027780102	0.01		
207520_at	-0.936622132674122	0		
213979_s_at	-0.935519171149618	0		CTBP1
229745_x_at	-0.93424475879621	0.01		
216680_s_at	-0.934196756237652	0		EPHB4
202572_s_at	0.924395823520243	0		KIAA0964
243228_at	0.916138491705783	0		

ALL B not Ph vs. T-ALL		samples: 9 / 9		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
242292_at	-3.53231266693437	0*	19.4	
36566_at	2.04687603382912	0		CTNS
230636_s_at	1.96129371358941	0		BTEB1
266_s_at	1.95685220231101	0		CD24
209771_x_at	1.95325312023269	0		CD24
219631_at	-1.90940390225071	0		FLJ12929
202113_s_at	1.86969444770264	0		SNX2
216379_x_at	1.84446878357139	0		
221969_at	1.82924887172424	0		PAX5
229487_at	1.78170685853126	0		
208650_s_at	1.77571318786079	0		CD24
218464_s_at	-1.71465707824422	0		FLJ10700
213944_x_at	1.69297405468728	0		
226496_at	1.65125933296341	0		
202206_at	-1.58502966518677	0		ARL7
205504_at	1.58481348793145	0		BTK
213539_at	-1.56405807954932	0		CD3D
211101_x_at	1.55958748994576	0.01		LILRA2
244876_at	1.55727218904507	0		
209772_s_at	1.54041193817483	0		CD24

ALL B not Ph vs. AML +8		samples: 9 / 10		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
229253_at	-2.32958521030012	0		CTMP
230441_at	2.03717805375485	0		
202382_s_at	-2.02017770346207	0		GNPI
209135_at	-1.93398721370049	0		ASPH
229487_at	1.78170685853126	0		
236656_s_at	1.74257382856431	0		
206438_x_at	-1.68325155133202	0		FLJ12975
207403_at	-1.66596170819766	0		IRS4
219615_s_at	-1.66280630807372	0		KCNK5
51192_at	-1.66236513015575	0		SSH-3
208248_x_at	-1.64870519570629	0*	1987.65	APLP2
218109_s_at	-1.60915618696108	0		FLJ14153
206295_at	-1.5980305395866	0		IL18
219013_at	-1.59551449458991	0		FLJ21634
217979_at	1.59385936644152	0		NET-6
208674_x_at	-1.58849840915584	0		DDOST
213474_at	1.58394324440508	0		
218351_at	-1.58117397105311	0		FLJ20502
235422_at	1.57754106652849	0		FALZ
227709_at	1.573035497361	0		RCN1

ALL B not Ph vs. AML

complex	samples: 9 / 36				
accuracy	1				
confidence	0.975685516889171				
gene	signal-to-noise	p	decision limit	gene symbol	
230441_at	2.03717805375485	0	584.1		
218168_s_at	-1.58072460849855	0*		CABC1	
219615_s_at	-1.55121221944569	0		KCNK5	
200620_at	-1.52004960803633	0		C1orf8	
229487_at	1.50364388130017	0			
218718_at	-1.4701929847603	0		PDGFC	
203372_s_at	1.43481740588652	0		STAT12	
205997_at	-1.40495787127453	0		ADAM28	
221969_at	1.3801763712428	0		PAX5	
209628_at	-1.36215023734312	0		P15-2	
243362_s_at	1.346548683162	0		LEF1	
219362_at	-1.34586251735194	0		FLJ22643	
244876_at	1.32930450347737	0			
227038_at	-1.3285550634404	0			
215001_s_at	-1.31302949268385	0		GLUL	
202382_s_at	-1.31028007399306	0		GNPI	
211574_s_at	-1.27970708025177	0		MCP	
203373_at	1.2683089746763	0		STAT12	
206847_s_at	-1.25861755739009	0		HOXA7	
90610_at	0.53320359867076	0.01		LRRN1	

ALL B not Ph vs. AML normal samples: 9 / 62

accuracy 0.985915492957746

confidence 1

failed: 51

gene	signal-to-noise	p	decision limit	gene symbol
230441_at	1.6244512124777	0		
229487_at	1.5789226463723	0		
244876_at	1.55727218904507	0		
230659_at	1.54315361034532	0		KIAA0212
214651_s_at	-1.46222218442109	0		HOXA9
221969_at	1.45958458157821	0*	695.5	PAX5
222915_s_at	1.43752454061174	0		BANK
204215_at	1.3973053569742	0		MGC4175
223469_at	-1.39620868523075	0		MGC10812
205997_at	-1.3950951014202	0		ADAM28
229253_at	-1.35885129348099	0		CTMP
209905_at	-1.35690502004825	0		HOXA9
236656_s_at	1.33665521300451	0		
205382_s_at	-1.33068263294683	0		DF
214761_at	1.3284704024734	0		OAZ
235753_at	-1.3151317291794	0		
218351_at	-1.29563799307181	0		FLJ20502
243362_s_at	1.29364059417566	0		LEF1
201482_at	-1.28902191317183	0		QSCN6
217979_at	1.28815999568218	0		NET-6

ALL B not Ph vs. AML t(8;21)		samples: 9 / 13			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
202382_s_at	-2.19898458962526	0*	48.7	GNPI	
230441_at	2.03717805375485	0			
228827_at	-2.03460798747208	0			
219478_at	-1.99876002437156	0		WFDC1	
218718_at	-1.92298631566524	0		PDGFC	
203795_s_at	1.88483347573406	0		BCL7A	
229487_at	1.78170685853126	0			
241383_at	-1.74636612447809	0			
236656_s_at	1.74257382856431	0			
235818_at	-1.70111545046162	0			
239278_at	1.69632987254595	0			
204647_at	-1.69400429479148	0		HOMER-3	
213944_x_at	1.69297405468728	0			
217989_at	-1.69293289781308	0		LOC51170	
205528_s_at	-1.64467496425566	0		CBFA2T1	
38269_at	1.6387714295779	0		PKD2	
201644_at	1.59860594123581	0		TSTA3	
206622_at	-1.58757343463781	0		TRH	
204319_s_at	-1.57313966435531	0		RGS10	

ALL Ph vs. all other		samples: 15 / 254		
accuracy	0.973977695167286			
confidence	1			
failed:	5,6,10,12,13,14,139			
gene	signal-to-noise	p	decision limit	gene symbol
210487_at	1.46744760454294	0		DNTT
203373_at	1.40251061555498	0		STAT12
234107_s_at	-1.30126819904145	0		
224772_at	1.2067398887062	0		MGC14961
201540_at	1.17259032247018	0		FHL1
202123_s_at	1.11803958640816	0		ABL1
202052_s_at	1.1015960943329	0		RAI14
207971_s_at	1.09522659077439	0		KIAA0582
218589_at	1.08650464406846	0		P2Y5
210299_s_at	1.08531672501274	0		FHL1
227584_at	1.05386625392045	0		
223314_at	1.04772672325566	0		MGC11352
203355_s_at	1.04604188199321	0		KIAA0942
212975_at	1.04561133965056	0		KIAA0870
214505_s_at	1.03851430654898	0		FHL1
222154_s_at	1.03658126355559	0		DKFZP564A2416
209679_s_at	1.00639728893477	0		LOC57228
230659_at	1.0054326445936	0		KIAA0212
1007_s_at	1.00231733413632	0		DDR1
227998_at	0.995615703854239	0*	3687.45	MGC17528

ALL Ph vs. T-ALL		samples: 15 / 9			
accuracy	1				
confidence	1				
gene	signal-to-noise	p	decision limit	gene symbol	
218224_at	-2.4418494296856	0		PNMA1	
213854_at	2.14963630962421	0		SYNGR1	
221969_at	2.06978634038245	0*	152.35	PAX5	
205101_at	1.84182814954198	0		MHC2TA	
213539_at	-1.83994967875006	0		CD3D	
228988_at	-1.79658055608971	0		ZNF6	
208894_at	1.79489847703276	0		HLA-DRA	
209604_s_at	-1.75648531255811	0		GATA3	
209619_at	1.72743796589982	0		CD74	
209771_x_at	1.69086499548436	0		CD24	
210982_s_at	1.68104679025052	0		HLA-DRA	
229487_at	1.66237077940113	0			
235706_at	1.65050775066494	0		CPM	
226878_at	1.64629305544324	0			
219631_at	-1.6447182870532	0		FLJ12929	
216379_x_at	1.61950446576807	0			
232234_at	-1.6009007845449	0		C20orf24	
210116_at	-1.58593866198308	0		SH2D1A	
224772_at	1.58464619249453	0		MGC14961	
213944_x_at	1.58085800202538	0			

ALL Ph vs. AML +8		samples: 15 / 10		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
210487_at	2.5237441884906	0		DNTT
203373_at	1.87201491464778	0		STAT2
202626_s_at	-1.85118734150368	0		LYN
226545_at	1.80654821675707	0		
219229_at	-1.75947760308609	0		SLC21A11
201828_x_at	-1.75807186867031	0		CXX1
217979_at	1.75748092515514	0		NET-6
51192_at	-1.7460030120736	0		SSH-3
229302_at	1.73677596348294	0		
226438_at	-1.70384127791425	0		
227367_at	-1.69193353561271	0		
229487_at	1.66237077940113	0		
234107_s_at	-1.64136875764363	0*	340.6	
204672_s_at	-1.64125970689002	0		ANKRD6
202625_at	-1.61126391589076	0		LYN
231887_s_at	1.60675392068253	0		KIAA1274
218942_at	-1.59127524427508	0		FLJ22055
210749_x_at	1.58213182698513	0		DDR1
213150_at	-1.57881564631984	0		HOXA10
59697_at	1.03007856466368	0		

ALL Ph vs. AML complex		samples: 15 / 36		
accuracy	0.980392156862745			
confidence	1			
failed:	41			
gene	signal-to-noise	p	decision limit	gene symbol
203373_at	2.31025004347829	0	250.95	STATI2
206847_s_at	-1.68023930751716	0		HOXA7
203372_s_at	1.63947005879125	0		STATI2
234107_s_at	-1.61839900546276	0		
210487_at	1.52754184797369	0		DNTT
214651_s_at	-1.49910544616071	0*		HOXA9
209619_at	1.49461107113623	0		CD74
218718_at	-1.42002659230416	0		PDGFC
225660_at	1.39520949215218	0		SEMA6A
226878_at	1.38541949367152	0		
235753_at	-1.36744735557489	0		
229817_at	1.35899260632582	0		DKFZP434M098
229487_at	1.334779526707	0		
214761_at	1.33168680907428	0		OAZ
225782_at	-1.32289994708003	0		
209905_at	-1.31131029251837	0		HOXA9
235521_at	-1.3094635283322	0		HOXA3
221969_at	1.30539974000703	0		PAX5
213150_at	-1.28908316992088	0		HOXA10
243363_at	1.22268997650812	0		LEF1

ALL Ph vs. AML normal		samples: 15 / 62			
accuracy	1				
confidence	0.974929287250918				
gene	signal-to-noise	p	decision limit	gene symbol	
214651_s_at	-1.85202940734635	0*	143.55	HOXA9	
203373_at	1.62915723435284	0		STAT12	
234107_s_at	-1.59102595714414	0			
229817_at	1.58719561744707	0		DKFZP434M098	
235753_at	-1.57582123676185	0			
224772_at	1.55894528337306	0		MGC14961	
210487_at	1.55488151717647	0		DNTT	
212012_at	1.4856092975255	0		D2S448	
223449_at	1.48450202420019	0		SEMA6A	
209905_at	-1.46906077761321	0		HOXA9	
213150_at	-1.46604197311664	0		HOXA10	
212975_at	1.45775514780451	0		KIAA0870	
221969_at	1.42534915280476	0		PAX5	
206847_s_at	-1.42447895990314	0		HOXA7	
214761_at	1.42199062015385	0		OAZ	
229487_at	1.42117416701658	0			
217979_at	1.40224984357617	0		NET-6	
225660_at	1.39520949215218	0		SEMA6A	
212013_at	1.38743332601863	0*	595.1	D2S448	
223314_at	1.38610020402626	0		MGC11352	

ALL Ph vs. AML t(8;21)		samples: 15 / 13		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
210487_at	2.25266231447204	0		DNTT
203373_at	2.24099300433703	0		STAT12
228827_at	-2.03460798747208	0*	162.15	
226545_at	1.91066898371188	0		
224928_at	1.88688841526862	0		
218718_at	-1.86717048634787	0		PDGFC
221581_s_at	1.85128137775803	0		WBSCR5
201811_x_at	1.82001958474325	0		SH3BP5
201486_at	1.78302051564335	0		RCN2
207655_s_at	1.77674162168543	0		BLNK
223467_at	1.77014181133384	0		RASD1
224764_at	1.76474506640734	0		ARHGAP10
218237_s_at	1.7513955350881	0		SLC38A1
212535_at	1.73463136017207	0		
202123_s_at	1.72757337414589	0		ABL1
50221_at	1.71143815565141	0		
202600_s_at	1.69190236878682	0		NRIP1
208146_s_at	1.67349162864443	0		CPVL
210151_s_at	1.66867162916475	0		DYRK3
229487_at	1.66237077940113	0		

T-ALL vs. all other

samples: 9 / 260

accuracy 0.988847583643123

confidence 0.974096654425726

failed: 2,8,239

gene	signal-to-noise	p	decision limit	gene symbol
213539_at	1.47540002688666	0		CD3D
230588_s_at	1.40173530720654	0		MCPR
209604_s_at	1.29998211445613	0*	1756.45	GATA3
233589_x_at	-1.29177430222739	0*	1	
201416_at	1.28847513298777	0		SOX4
228988_at	1.22715826655642	0		ZNF6
205640_at	-1.20119307753531	0		ALDH3B1
201417_at	1.20045529988474	0		
228174_at	1.19343398440307	0		
206804_at	1.19196138585152	0		CD3G
218913_s_at	-1.18780274620161	0		LOC51291
221188_s_at	-1.17857568967097	0		CIDEB
221555_x_at	-1.15605774789743	0		CDC14B
229280_s_at	1.14891159995685	0		
219079_at	-1.1401640005663	0		b5&b5R
228242_at	1.13931660332537	0		
225003_at	-1.13574793214416	0		MBC3205
205504_at	-1.1269796752374	0		BTK
209499_x_at	-1.12273253976539	0		TNFSF13
226342_at	1.11835127434314	0		

T-ALL vs. AML +8		samples: 9 / 10		
accuracy	1			
confidence	1			
gene	signal-to-noise	p	decision limit	gene symbol
233589_x_at	-5.40566971880279	0*	94.05	
211495_x_at	-3.24639126977955	0		TNFSF13
209499_x_at	-2.48173374690971	0		TNFSF13
201416_at	2.45175574451932	0		SOX4
227999_at	-2.41422896946156	0		LOC170394
205640_at	-2.36735951723515	0		ALDH3B1
218913_s_at	-2.26146566262815	0		LOC51291
242292_at	2.13276982228889	0		
227729_at	2.11399761533966	0		
206295_at	-2.10263843038377	0		IL18
218341_at	-2.09693358964157	0		FLJ11838
217989_at	-2.01015824384982	0		LOC51170
201200_at	-1.9921136873539	0		CREG
202626_s_at	-1.97579203488485	0		LYN
201417_at	1.94726816387174	0		
201985_at	-1.9229605331952	0		KIAA0196
219013_at	-1.91889126390119	0		FLJ21634
219329_s_at	-1.91383490407803	0		APR-3
230588_s_at	1.87407116981284	0		MCPR
39650_s_at	1.68662830524108	0		KIAA0435

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